

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:02:08 ; Search time 69.9874 Seconds
(without alignments)
235.865 Million cpi1 updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTKLFEPTBECNGYVAGEE.....CPNLHKQGYANQNGRC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : 1-Geneseq_19Jun03.*

- 1: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1980.DAT.*
- 2: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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- 22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
- 23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
- 24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	696	21	AA54457
2	630	100.0	696	22	AAU07190
3	630	100.0	696	23	AB878130
4	630	100.0	832	20	AA530207
5	630	100.0	832	20	AA525120
6	630	100.0	832	24	AB47778
7	630	100.0	832	24	ABU56479
8	630	100.0	832	24	ABU56563
9	586	93.0	540	22	AAE13059

10	404.5	64.2	488	16	AAE67757	Human fetal brain
11	404.5	64.2	524	16	AAE67758	Human fetal brain
12	404.5	64.2	524	16	AAE67759	Human fetal brain
13	404.5	64.2	769	16	AAE7352	Human fetal brain
14	363.5	57.7	823	20	AAE25119	Human MDC2-beta pr
15	363.5	57.7	859	20	AAE25118	Human MDC2-alpha p
16	363.5	57.7	867	20	AAE30208	Amino acid sequenc
17	338.5	53.7	542	22	AAE13058	ADAM-22dis-Fc fusi
18	292	46.3	686	23	AAO14360	Human metalloprote
19	292	46.3	802	23	AAE47105	First splice varia
20	292	46.3	802	23	ABE78239	Amino acid sequenc
21	292	46.3	812	22	ABE00942	Gene 216 alternati
22	292	46.3	812	22	AAE47106	Second splice vari
23	292	46.3	812	23	ABE78300	Amino acid sequenc
24	292	46.3	812	23	AAU98885	Human protease PR
25	292	46.3	812	23	AAO14377	Human metalloprote
26	292	46.3	812	24	ABU55870	Human 216 protein
27	292	46.3	813	22	AAU29256	Human PRO polypept
28	292	46.3	813	24	ABU71344	Human PRO1891 prot
29	292	46.3	813	24	ABU65801	Human secreted/cra
30	292	46.3	813	24	ABU66134	Human secreted/cra
31	292	46.3	813	24	ABU67638	Human secreted/cra
32	292	46.3	813	24	ABU65496	Human PRO polypept
33	292	46.3	813	24	ABU58632	Human secreted/cra
34	292	46.3	813	24	ABU56168	Human secreted/cra
35	292	46.3	813	24	ABU57163	Human PRO polypept
36	292	46.3	813	24	ABU10742	Human secreted/cra
37	292	46.3	826	22	ABE00926	Gene 216 polypept
38	292	46.3	826	24	ABU55849	Human gene 216 pro
39	292	46.3	874	23	ABU10599	Human novel protei
40	292	46.3	882	23	AAU72898	Human metalloprote
41	292	46.3	895	23	ABU10598	Human novel protei
42	292	46.3	914	23	ABU10597	Human novel protei
43	279	44.3	522	22	AAE13054	ADAM-15dis-Fc fusi
44	278	44.1	709	17	AAE9801	CR11-7 nerve prote
45	276.5	43.9	1569	22	ABE63422	Drosophila melanog

ALIGNMENTS

RESULT 1	
AA54457	
ID	AA54457 standard; Protein: 696 AA.
XX	
AC	AA54457;
XX	
DT	25-APR-2000 (first entry)
XX	
DE	Amino acid sequence of a disintegrin homologue designated zdin1.
XX	
KW	Human, disintegrin homologue; zdin1; cardiac myocyte; adipocyte;
KW	gene therapy; cell-cell interaction; chondro sarcoma; atherosclerosis;
KW	Alzheimer's disease; restenosis; ischemic reperfusion; obesity;
KW	intimal hyperplasia; tumour; platelet aggregation; apoptosis;
KW	neurogenesis; myogenesis; arthritis; myogenesis; neurogenesis;
KW	connective tissue disorder; chondrogenesis; tumour proliferation;
KW	inflammation.
XX	
OS	Homo sapiens.
XX	
Key	Location/Qualifiers
FT	Domain 1..163
FT	/note= "propeptide sequence"
FT	Domain 164..382
FT	/note= "protease sequence; this sequence is specifically claimed in claim 4"
FT	Domain 383..464
FT	/note= "disintegrin sequence; this sequence is specifically claimed in claim 5"
FT	Misc-difference 437..450
FT	/note= "this sequence is specifically claimed in claim 2"
FT	Region 438..449

```
FT      /note="disintegrin loop"
FT      Region
FT      443..445
FT      /note="RGD binding loop"
FT      465..696
FT      Domain
FT      /note="cysteine-rich domain; this sequence is
FT      specifically claimed in claim 6"
XX
XX      WO200002912-A2.
XX
XX      20-JAN-2000.
XX
XX      09-JUL-1999; 99WO-US15638.
XX
XX      10-JUL-1998; 98US-0113883.
XX
XX      (Zymo ) ZYMOGENETICS INC.
XX
XX      Shepard PO, Bairdur N, Deisher TA, Bishop PD,
XX
XX      WPI; 2000-160898/14.
XX      N-PSDB; AA245826.
XX
XX      Polypeptide useful in modulating cell-cell interaction in tissues of
XX      heart, brain, spinal cord and treating chondro sarcoma,
XX      atherosclerosis, restenosis, obesity, intimal hyperplasia and tumors -
XX
XX      Claim 7; Page 127-129; 132pp; English.
XX
XX      The present sequence represents a human disintegrin homologue, designated
XX      zdin1. The zdin1 polypeptide is a cardiac myocyte proliferation and
XX      differentiation stimulator, as well as an adipocyte proliferation and
XX      differentiation inhibitor. Polynucleotides encoding zdin1 are used in
XX      gene therapy. The zdin1 polypeptide is useful in modulating cell-cell
XX      interactions of cells derived from tissues of heart, brain, spinal cord
XX      and skeletal muscle. It is useful in treating and diagnosing chondro
XX      sarcoma, atherosclerosis, Alzheimer's disease, restenosis, ischemic
XX      reperfusion, obesity, intimal hyperplasia and tumors of heart, brain,
XX      and spinal cord. The zdin1 polypeptide is also useful in identifying
XX      its new family members, antagonists, agonists and antibodies.
XX      Antagonists, antibodies and fusion proteins of zdin1 are useful in
XX      inhibiting platelet aggregation, apoptosis, neurogenesis and myogenesis.
XX      Agonists and antagonists are useful in studying cell-cell interactions,
XX      arthritis, myogenesis, neurogenesis, connective tissue disorders,
XX      chondrogenesis, tumour proliferation and suppression, extracellular
XX      matrix proteins, repair and remodelling of ischemic reperfusion,
XX      inflammation, and apoptosis.
XX
XX      Sequence 696 AA;
SQ
Query Match 100.0%; Score 630; DB 21; Length 696;
Best Local Similarity 100.0%; Pred. No. 1e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 PTKLEPPTCGNGYVAGEECDCGFHVECYGLCKCKCSLSNGAHGSDGPCNNNTSCLFOP 60
DB      373 PTKLEPPTCGNGYVAGEECDCGFHVECYGLCKCKCSLSNGAHGSDGPCNNNTSCLFOP 432
OY      61 RGYECRDVAVNECDITEYCTGDSGQCPNTHKODGYACNONGRC 104
DB      433 RGYECRDVAVNECDITEYCTGDSGQCPNTHKODGYACNONGRC 476
XX
XX      RESULT 2
XX      AAU07190
XX      ID AAU07190 strand; Protein; 696 AA.
XX
XX      AAU07190;
XX
XX      04-DEC-2001 (first entry)
XX
XX      Human disintegrin protease, zdin1.
XX
XX      Human; disintegrin; zdin1; antiangiogenic; vascular; thrombolytic.
XX
XX      KM
```

```
KW      cell matrix; cell-cell interactions; apoptosis; neurogenesis;
KW      connective tissue disorders; chondrogenesis; arthritis;
KW      tumour proliferation; ischaemia reperfusion; inflammation;
KW      chromosome 2q33.
XX
XX      Homo sapiens.
XX
XX      Key
XX      Location/Qualifiers
XX      1..163
XX      /label= Propeptide
XX      164..696
XX      /label= Mature zdin1
XX      /note="This sequence is specifically claimed in
XX      claim 4"
XX      164..382
XX      /label= Protease_region
XX      /note="This sequence is specifically claimed in
XX      claim 1"
XX      383..464
XX      /label= Disintegrin sequence
XX      /note="This sequence is specifically claimed in
XX      claim 2"
XX      383..696
XX      /label= Disintegrin/cysteine rich sequence
XX      /note="This sequence is specifically claimed in
XX      claim 3"
XX      438..449
XX      /label= Disintegrin_loop
XX      443..445
XX      /label= RGD_binding_loop
XX
XX      Binding-site
XX
XX      US6265199-B1.
XX
XX      24-JUL-2001.
XX
XX      09-JUL-1999; 99US-0351414.
XX
XX      10-JUL-1998; 98US-0092371.
XX
XX      (Zymo ) ZYMOGENETICS INC.
XX
XX      Shepard PO, Bairdur N, Deisher TA, Bishop PD, Taft DW;
XX
XX      WPI; 2001-450736/48.
XX      N-PSDB; AAS11991.
XX
XX      Disintegrins protease zdin1, useful for producing agents for the
XX      development of antithrombotic and anti-migration of tumour cells and
XX      have antiangiogenic activity -
XX
XX      Claim 5; Column 53-56; 50pp; English.
XX
XX      The invention relates to an isolated novel disintegrin protease family
XX      member, zdin1. Disintegrins bind cell surface molecules, including
XX      integrins, on the surface of various cells such as platelets,
XX      fibroblasts, tumour, endothelial, muscle, neuronal, bone and sperm cells.
XX      Disintegrins are unique and potentially useful tools for investigating
XX      cell matrix and cell-cell interactions, apoptosis, neurogenesis,
XX      connective tissue disorders, chondrogenesis, arthritis, tumour
XX      proliferation, ischaemia reperfusion and inflammation. Additionally, they
XX      are useful in the development of antithrombotic and anti-migration of
XX      tumour cells and have antiangiogenic activity. The present sequence
XX      represents human disintegrin, zdin1, the gene for which is located on
XX      chromosome 2q33.
XX
XX      Sequence 696 AA;
SQ
Query Match 100.0%; Score 630; DB 22; Length 696;
Best Local Similarity 100.0%; Pred. No. 1e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY      1 PTKLEPPTCGNGYVAGEECDCGFHVECYGLCKCKCSLSNGAHGSDGPCNNNTSCLFOP 60
XX
XX      KM
```

Db 373 PTKLFEPTGCGNGVYAGEBDCGFHVECYGLCKKCSLSNGAHCSDGPCNNTSCLFQP 432
 QY 61 RGYECRDVAVNECDITEYCTGDSGGCPNLLHKQDGYACNONGRC 104
 433 RGYECRDVAVNECDITEYCTGDSGGCPNLLHKQDGYACNONGRC 476
 Db 433 RGYECRDVAVNECDITEYCTGDSGGCPNLLHKQDGYACNONGRC 476
 RESULT 3
 ABB78130
 ID ABB78130 standard; Protein; 696 AA.
 AC ABB78130;
 XX
 DT 05-NOV-2002 (first entry)
 XX
 DE Amino acid sequence of human zdin1.
 XX
 KW Human; zdin1; disintegrin protease; platelet accumulation;
 KW chromosome 2q33; platelet aggregation; proteolysis; apoptosis;
 KW neurogenesis; myogenesis; connective tissue disorder; arthritis;
 KW chondrogenesis; cell adhesion; cell fusion; neuron; myocyte; heart;
 KW brain; spinal cord; skeletal muscle tissue; Alzheimer's disease;
 KW tumour formation; multiple sclerosis; congestive heart failure;
 KW ischaemic reperfusion; intimal hyperplasia; restenosis; enzyme.
 KW
 XX Homo sapiens.
 OS
 XX
 Key Location/Qualifiers
 FH Domain 164..382
 FT /note="protease domain"
 FT 383..464
 FT Domain /note="disintegrin sequence"
 FT Region 438..449
 FT /note="disintegrin loop"
 FT 465..696
 FT Domain /note="cystein-rich domain"
 FT
 XX
 XX US2002072102-A1.
 XX
 XX 13-JUN-2002.
 PD
 XX 16-MAR-2001; 2001US-0809790.
 XX
 PF 10-JUL-1998; 98US-092371P.
 PR 09-JUL-1999; 99US-0351414.
 XX
 XX (SHEP/) SHEPPARD P O.
 PA (BAIN/) BAINDUR N.
 PA (DEIS/) DEISHER T A.
 PA (BISH/) BISHOP P D.
 XX
 PI Sheppard PO, Bainsdur N, Deisher TA, Bishop PD;
 DR WPI: 2002-598452/64.
 DR N-PSDB; ABO78447.
 XX
 PT New disintegrin homolog polypeptide and polynucleotide, useful for
 PT modulating cell-cell interactions and diagnosis, treatment of
 PT Alzheimer's disease, tumour formation, multiple sclerosis and congestive
 PT heart failure
 PT
 XX
 PS Claim 7; Page 29-30; 53pp; English.
 XX
 CC The present sequence represents a human polypeptide designated zdin1.
 CC zdin1 is a member of the disintegrin protease family. Zdin1 inhibits
 CC platelet accumulation. The zdin1 gene is present on chromosome 2q33.
 CC Zdin1 polypeptides and polynucleotides are useful in treatment of
 CC disorders associated with infarct in brain or heart tissue and/or
 CC platelet aggregation, to modulate proteolysis, apoptosis, neurogenesis,
 CC myogenesis, connective tissue disorders, arthritis, chondrogenesis,
 CC cell adhesion, cell fusion, and signalling or to treat or prevent
 CC development of pathological conditions in such diverse tissue as heart,
 CC brain, spinal cord and skeletal muscle. The molecules modulate

CC inhibition and proliferation of neurons and myocytes in heart, brain,
 CC spinal cord and skeletal muscle tissue. Disorders which may be amenable
 CC to diagnosis, treatment or prevention with zdin1 polypeptides include,
 CC Alzheimer's disease, tumour formation, multiple sclerosis, congestive
 CC heart failure, ischaemic reperfusion or infarct and degenerative
 CC diseases. The zdin1 molecules particularly useful in the treatment of
 CC intimal hyperplasia or restenosis due to acute vascular injury.
 CC
 XX
 SQ Sequence 696 AA;
 Query Match 100.0%; Score 630; DB 23; Length 696;
 Best Local Similarity 100.0%; Pred. No. 1e-42;
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 PTKLFEPTGCGNGVYAGEBDCGFHVECYGLCKKCSLSNGAHCSDGPCNNTSCLFQP 60
 Db 373 PTKLFEPTGCGNGVYAGEBDCGFHVECYGLCKKCSLSNGAHCSDGPCNNTSCLFQP 432
 QY 61 RGYECRDVAVNECDITEYCTGDSGGCPNLLHKQDGYACNONGRC 104
 433 RGYECRDVAVNECDITEYCTGDSGGCPNLLHKQDGYACNONGRC 476
 Db 433 RGYECRDVAVNECDITEYCTGDSGGCPNLLHKQDGYACNONGRC 476
 RESULT 4
 AAY30207
 ID AAY30207 standard; Protein; 832 AA.
 XX
 AC AAY30207;
 XX
 DT 29-OCT-1999 (first entry)
 XX
 DE Amino acid sequence of the human SVP3-17 protein.
 XX
 KW SVP3-17; metalloproteinase-disintegrin; human chromosome 2;
 KW human chromosome 7; malignant hyperthermia susceptibility;
 KW Zellweger syndrome; neonatal adrenoleukodystrophy;
 KW infantile Refsum disease; progressive familial intrahepatic cholestasis;
 KW mucopolysaccharidosis VII; split hand/foot malformation;
 KW arylphymogenic right ventricular dysplasia-4; Coppock-like cataract;
 KW insulin dependent diabetes mellitus-12; lamellar type ichthyosis;
 KW transient neonatal myaesthesia gravis; congenital aculeiform cataract;
 KW juvenile amyotrophic lateral sclerosis;
 KW familial paroxysmal choreoathetosis;
 KW Finnish lethal neonatal metabolic syndrome.
 KW
 XX Homo sapiens.
 OS
 XX
 XX WO9941388-A2.
 XX
 PD 19-AUG-1999.
 PD
 XX 11-FEB-1999; 99WO-US03016.
 PF 11-FEB-1999;
 PR 11-FEB-1998; 98US-0074310.
 XX
 XX (IMMV) IMMUNEX CORP.
 PA
 XX Cerretti DP;
 PI
 XX WPI: 1999-527371/44.
 DR N-PSDB; AA210207.
 DR
 XX
 PT DNA encoding the SVP3-13 and SVP3-17 proteins for detecting
 PT disease corresponding to chromosome 7, e.g. Zellweger syndrome
 PT
 XX
 PS Claim 1; Page 8-9; 82pp; English.
 XX
 CC The present sequence represents a protein designated SVP3-17, which
 CC is a member of the metalloproteinase-disintegrin family. The
 CC specification also describes SVP3-13 proteins. Both sequences can
 CC be used to identify human chromosome 2 or 7, and to map genes on these
 CC two chromosomes, and also to identify genes associated with certain
 CC diseases, syndromes, or other human conditions associated with human

CC chromosome 2 or 7. The disease that correspond to chromosome 7 include
CC malignant hyperthermia susceptibility, Zellweger syndrome, neonatal
CC adrenoleukodystrophy, infantile Refsum disease, progressive familial
CC intrahepatic cholestasis, mucopolysaccharidosis VII, and split
CC hand/foot malformation. Diseases associated with chromosome 2 include
CC arrhythmogenic right ventricular dysplasia-4, insulin dependent diabetes
CC mellitus-12, transient neonatal myasthenia gravis, juvenile amyotrophic
CC lateral sclerosis, congenital aequileiform cataract, Copcock-like cataract,
CC lamellar type ichthyosis, familial paroxysmal choreoathetosis, and
CC Finnish lethal neonatal metabolic syndrome.

XX
SQ Sequence 832 AA;

Query Match 100.0%; Score 630; DB 20; Length 832;
Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFQP 60

DB 496 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFQP 555

QY 61 RGYECRDVNECDITREYCTGDSGQCPNLIHKODGYACNONGRC 104

DB 556 RGYECRDVNECDITREYCTGDSGQCPNLIHKODGYACNONGRC 599

RESULT 5

AAV25120 standard; Protein; 832 AA.

XX AAV25120;

DT 26-AUG-1999 (first entry)

XX Human MDC3 protein.

KW Metalloproteinase-like-disintegrin-like cysteine rich protein; human;

XX MDC2-alpha; MDC2-beta; MDC3; medical; treatment; diagnosis.

OS Homo sapiens.

PN JP1155574-A.

XX 15-JUN-1999.

PF 01-DEC-1997; 97JP-0330020.

PR 01-DEC-1997; 97JP-0330020.

XX (EISA) EISAI CO LTD.

PA WPI: 1999-398071/34.

DR N-PSDB; AAI78438.

XX New protein belonging to MDC gene family - useful in medical

PT treatment and diagnosis

XX Disclosure: Page 13-16; 17pp; Japanese.

CC This invention describes novel human MDC2-alpha, MDC2-beta and MDC3

CC proteins and their encoding nucleic acids. The products of the invention

CC are useful in medical treatment and diagnosis.

XX Sequence 832 AA;

QY 1 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFQP 60

DB 496 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFQP 555

QY 61 RGYECRDVNECDITREYCTGDSGQCPNLIHKODGYACNONGRC 104

DB 556 RGYECRDVNECDITREYCTGDSGQCPNLIHKODGYACNONGRC 599

RESULT 6

AAV47778 standard; Protein; 832 AA.

XX AAV47778;

DT 04-MAR-2002 (first entry)

XX ADAM 23.

KW Disintegrin; ADAM 23; metalloproteinase; domain; adhesion; proteolysis;

XX modulator; alpha-v-beta3 integrin; tumour progression; neural tissue;

OS Homo sapiens.

XX Key Location/Qualifiers

FT Domain 563..570

XX /Label= Disintegrin domain

PN WO200174857-A2.

XX 11-OCT-2001.

PF 02-APR-2001; 2001WO-US10729.

PR 03-APR-2000; 2000US-194164P.

XX (BRIM) BRISTOL-MYERS SQUIBB CO.

PI Lopez-Otin C, Freilji JMP, Bianchi AB, Miguel SC, Garcia JML;

XX Trail P;

DR WPI: 2002-066298/09.

XX N-PSDB; AAI72025.

XX Nucleic acid encoding a new ADAM family member, designated ADAM 23 is

PT useful to find modulators of its interaction with integrin which can be

XX used to prevent angiogenesis or increase neural growth -

PS Disclosure: Page 38-41; 44pp; English.

CC This sequence shows a cellular disintegrin, ADAM 23, which is a

CC protein having a disintegrin and metalloproteinase domain. This

CC protein can perform both adhesion and proteolysis functions.

CC Modulators of the interaction between ADAM and alpha-v-beta3 integrin

CC are used to inhibit tumour progression or induce growth of neural

CC tissue. These compounds modulate angiogenesis and induction of matrix

CC metalloproteinases facilitating migration of tumour cells and growth of

XX neural tissue.

XX Sequence 832 AA;

QY 1 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFQP 60

DB 496 PTKLFPEPTCGNGYVAGEBCDCGFHVECYGLCKKCSLSNGAHCSGDPCCNNTSCLFQP 555

QY 61 RGYECRDVNECDITREYCTGDSGQCPNLIHKODGYACNONGRC 104

DB 556 RGYECRDVNECDITREYCTGDSGQCPNLIHKODGYACNONGRC 599

RESULT 7

ABU56479

ID ABUS6479 standard; Protein: 832 AA.
XX
AC ABUS6479;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #72.
XX
KW Lung cancer-associated polypeptide; cytosolic; emphysema;
KM antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN W0200286443-A2.
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US12476.
XX
PR 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI: 2003-093161/08.
DR N-PSDB; ABX76201.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
PS Claim 27; Page 243-244; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC polypeptides of the invention.
XX
SQ Sequence 832 AA;
XX
Query Match 100.0%; Score 630; DB 24; Length 832;
Beat Local Similarity 100.0%; Pred. NO. 1.2e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 PTKLFEPTGNGVAGEECDCGFHVCYGLCKKCKSLNSGARSDDPCCNNTSCLFOP 60
DB 496 PTKLFEPTGNGVAGEECDCGFHVCYGLCKKCKSLNSGARSDDPCCNNTSCLFOP 555

OY 61 RGYECRDVNECDITEXCTGDSGCCPPNHLKODGYACNOQGRG 104
DB 556 RGYECRDVNECDITEXCTGDSGCCPPNHLKODGYACNOQGRG 599
RESULT 8
ID ABUS6563 standard; Protein: 832 AA.
XX
AC ABUS6563;
XX
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polypeptide #156.
XX
KW Lung cancer-associated polypeptide; cytosolic; emphysema;
KM antiinflammatory; antiasthmatic; non-small cell lung cancer; atelectasis;
KM small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KM chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KM interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
XX
OS Unidentified.
XX
PN W0200286443-A2.
PD 31-OCT-2002.
XX
PF 18-APR-2002; 2002WO-US12476.
XX
PR 18-APR-2001; 2001US-284770P.
PR 10-MAY-2001; 2001US-290492P.
PR 09-NOV-2001; 2001US-339245P.
PR 13-NOV-2001; 2001US-350666P.
PR 29-NOV-2001; 2001US-334370P.
PR 12-APR-2002; 2002US-372246P.
XX
PA (EOSB-) EOS BIOTECHNOLOGY INC.
XX
PI Aziz N, Murray R;
XX
DR WPI: 2003-093161/08.
DR N-PSDB; ABX76292.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer -
XX
PS Claim 27; Page 308; 453pp; English.
XX
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung
CC cancer-associated polynucleotides and polypeptides are used for
CC identifying a compound that modulates a lung cancer-associated
CC polypeptide, for inhibiting proliferation of a lung cancer-associated
CC cell to treat lung cancer in a patient and for treating a mammal having
CC lung cancer by administering a modulatory compound identified. The
CC methods are useful for treating lung cancer, such as small cell lung
CC cancer, non-small cell lung cancer or other benign or precancerous
CC lesions, e.g. atelectasis, emphysema, bronchitis, chronic obstructive
CC pulmonary disease, fibrosis, hypersensitivity pneumonitis, interstitial
CC pulmonary fibrosis, asthma and bronchiectasis. The genes, polynucleotides
CC and polypeptides are useful for diagnostic purposes and as targets for
CC screening for therapeutic compounds that modulate lung cancer, such as
CC antibodies. Sequences ABUS6408-ABUS6745 represent lung cancer-associated
CC polypeptides of the invention.
XX
SQ Sequence 832 AA;
XX
Query Match 100.0%; Score 630; DB 24; Length 832;

Best Local Similarity 100.0%; Pred. No. 1.2e-42;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 PTKLEPPEPCNGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOP 60
|||||
DB 466 PTKLEPPEPCNGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOP 555
|||||

QY 61 RGYECRDVAINECDITEYCTGDSGOCPPNLHKODGYACNONOGRG 104
|||||
DB 556 RGYECRDVAINECDITEYCTGDSGOCPPNLHKODGYACNONOGRG 599
|||||

RESULT 9
AAE13059 standard; Protein; 540 AA.
ID AAE13059
XX AAE13059;
AC
XX
XX 28-JAN-2002 (first entry)
XX
XX
DE ADAM-23dis-Fc fusion construct.

Human; ADAM disintegrin domain; integrin; endothelial cell migration;
angiogenesis; ocular disorder; inflammatory disease; bone resorption;
osteoporosis; restenosis; thrombosis; tissue repair; wound healing;
retinopathy; retinoblastoma; neovascular glaucoma; macular degeneration;
retrolental fibroplasia; inflammatory bowel disease; rubecosis; uveitis;
arthritis; rheumatism; myocardial infarction; coronary artery disease;
tumour; stroke; atherosclerosis; arteriosclerosis; injury; psoriasis;
preclampsia; embolism; ischaemia; fusion construct; immunoglobulin K;
IgK; Fc region; antiinflammatory; osteopathic; vasolytic; thrombolytic.

OS Chimeric - Homo sapiens.
XX Chimeric - Unidentified.
XX
FH Key Location/Qualifiers
FT 1..20
FT Peptide /label= IgK_leader_sequence
FT Protein 21..540
FT /note= "Mature ADAM-23dis-Fc fusion construct"
FT Region 23..310
FT /note= "Human ADAM disintegrin"
FT Domain 34..91
FT /label= Human_ADAM_disintegrin_domain
FT Region 313..540
FT /note= "Fc region"

XX
XX WO200162905-A2.
XX
XX 30-AUG-2001.
XX
XX 23-FEB-2001; 2001WO-US05701.
XX
XX 25-FEB-2000; 2000US-184865P.
XX
XX (IMMUNEX CORP.
XX
XX Fanslow WC, Cerretti DP, Pointdexter KM, Black RA;
XX
XX WPI; 2001-625725/72.
XX
XX DR N-PSDB; AAD21439.
XX
XX Antagonizing the binding of an integrin to its ligand useful for the
XX treatment of angiogenesis comprises administration of an
XX ADAM-disintegrin domain polypeptide
XX
XX Claim 11; Page 60-61; 66p; English.
XX
XX The invention relates to the method and use of ADAM disintegrin domain
XX polypeptides for inhibiting the biological activity of integrins,
XX endothelial cell migration and angiogenesis. ADAM disintegrin domain
XX polypeptides are used for treatment of ocular disorders, malignant and
XX metastatic conditions, inflammatory diseases, osteoporosis and other

CC conditions mediated by accelerated bone resorption, restenosis,
CC inappropriate platelet activation, recruitment or aggregation, thrombosis
CC or a condition requiring aggregation, thrombosis or a condition requiring
CC tissue repair or wound healing, angiogenesis, ocular neovascularisation
CC or solid tumour, diabetic retinopathy, retinopathy or prematurity,
CC neovascular glaucoma, retinoblastoma, retrolental fibroplasias, rubecosis,
CC uveitis, macular degeneration and corneal graft neovascularisation,
CC inflammatory diseases, ocular tumours, diseases associated with choroidal
CC or iris neovascularisation, arthritis, rheumatism, inflammatory bowel
CC disease, psoriasis, coronary artery disease or injury, myocardial
CC infarction or injury following myocardial infarction, stroke, unstable
CC angina, atherosclerosis, arteriosclerosis, preclampsia, embolism,
CC platelet-associated ischaemic disorders including lung ischaemia,
CC coronary ischaemia, cerebral ischaemia, restenosis following percutaneous
CC coronary intervention including angioplasty, atherectomy, stent placement
CC and bypass surgery, thrombotic disorders including coronary artery
CC thrombosis, cerebral artery thrombosis, intracardiac thrombosis,
CC peripheral artery thrombosis, venous thrombosis, thrombosis and
CC coagulopathies associated with exposure to a foreign or injured tissue
CC surface and reocclusion following thrombosis, deep venous thrombosis,
CC pulmonary embolism, transient ischaemic attacks and another conditions
CC where vascular occlusion is a common underlying feature, in individuals
CC at high risk for thrombus formation of reformation, advanced coronary
CC artery disease, or for occlusion, reocclusion, stenosis and/or restenosis
CC of blood vessels or stroke benign tumours and preneoplastic conditions,
CC myocardial angiogenesis, haemophilic joints, scleroderma, vascular
CC adhesions, asthma and allergy, eczema and dermatitis, graft versus host
CC disease, sepsis, adult respiratory distress syndrome, telangiectasia and
CC wound granulation. The method are used in combination with angioplasty
CC procedures, such as balloon angioplasty, laser angioplasty, coronary
CC atherectomy or similar techniques, carotid endarterectomy, anastomosis of
CC vascular grafts, surgery having a high risk of thrombus formation (i.e.
CC coronary bypass surgery, insertion of a prosthetic valve or vessel and
CC the like), atherectomy, stent placement, placement of a chronic
CC cardiovascular device such as an in-dwelling catheter or prosthetic valve
CC or vessel, organ transplantation or bypass surgery. The present sequence
CC is ADAM disintegrin domain polypeptide fusion construct. The fusion
CC construct comprises of immunoglobulin K (IgK) leader, human ADAM
CC disintegrin and Fc region.

XX
XX SQ Sequence 540 AA;
XX
XX Query Match 93.0%; Score 586; DB 22; Length 540;
XX Best Local Similarity 99.0%; Pred. No. 2.8e-39;
XX Matches 96; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 TECNGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOPRGYECRD 67
|||||
DB 21 TSCGNGYVAGEBECDCGFHVECYGLCKKCSLSNAGHSDGPPCCNNTSCLFOPRGYECRD 80
|||||

QY 68 AVNECDITEYCTGDSGOCPPNLHKODGYACNONOGRG 104
|||||
DB 81 AVNECDITEYCTGDSGOCPPNLHKODGYACNONOGRG 117
|||||

RESULT 10
AAR67757
ID AAR67757 standard; Protein; 488 AA.
XX
XX AAR67757;
XX
XX 25-MAR-2003 (updated)
XX DT 01-AUG-1995 (first entry)
XX
XX Human fetal brain MDC protein.
XX
XX MDC protein; breast cancer; mamma carcinoma; ovary cancer;
XX chromosome-17.
XX
XX Homo sapiens.
XX
XX EP633268-A2.
XX

PD 11-JAN-1995.
 XX
 PF 13-MAY-1994; 94EP-0107487.
 XX
 PR 14-MAY-1993; 93JP-0136602.
 PR 22-SEP-1993; 93JP-0257455.
 PR 23-FEB-1994; 94JP-0049904.
 PR 12-APR-1994; 94JP-0073328.
 XX
 PA (CANC-) CANCER INST.
 PA (EISA) EISAI CO LTD.
 XX
 PI Emi M, Nakamura Y;
 XX
 XX WPI: 1995-038478/06.
 DR N-PSDB; AAQ76119.
 XX
 XX Novel MDC protein and DNA encoding it - used to develop prods.
 PT for the study, diagnosis and therapy of cancers, partic. breast
 PT and ovarian cancer
 XX
 PS Disclosure; Page 73-74; 123pp; English.
 CC A detailed map of human chromosome-17 was constructed to analyze the
 CC chromosome in breast and ovarian cancer tissues. 2 Novel cDNAs
 CC (given in AAQ76120-21) were obtained from fetal cerebellum that
 CC encoded novel MDC proteins (AAR67758-59, respectively). 5'-RACE and
 CC RT-PCR revealed the sequence given in AAQ76122, encoding the MDC given
 CC in AAR75352. Sequences common for these clones are given in AAQ76119
 CC and AAR66757, respectively. A genomic DNA sequence (AAQ76124) for MDC
 CC was obtained from cosmid clone CCl17-904.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 488 AA;
 QY Query Match 64.2%; Score 404.5; DB 16; Length 488;
 DB Best Local Similarity 65.4%; Pred. No. 8.8e-25;
 Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;
 QY 1 PTKLFEPTCCNGVVEAGEECDCGFHVECY--GLCCCKKSLNSGAGHSDGPCNNTSCL 57
 DB 332 PLKLDPEECGNGFVEAGEECDCGVSQCSRAGGNCCKKCTLTLDAMCSIDLCCRR--CK 389
 QY 58 FQPRGYECRDVAVNECDITREYCTGDSGCCPPNHLKODGYACNONOGR 104
 DB 390 YEPNGVSCRAVNECDIAETCTGDSGCCPPNHLKLDGYCDHEQGR 436

Search completed: October 21, 2003, 10:08:27
 Job time : 71.9874 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 10:00:20 ; Search time 29.424 Seconds
(without alignments)
339.796 Million call updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PTKLFEPTECGNGVGEAGE.....CPNHLKQDGYACNQNGRC 104

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404.5	64.2	524	S38539	disintegrin-like m
2	404.5	64.2	670	S60258	disintegrin-like m
3	283	44.9	617	S48160	metalloproteinase
4	274	43.5	814	G02390	disintegrin-like m
5	261	41.4	903	S60257	metcryn alpha - mo
6	255	40.5	419	A59414	metalloproteinase
7	255	40.5	571	S24789	metalloproteinase
8	255	40.5	609	S55270	metalloproteinase
9	254.5	40.4	357	S24403	carboxypeptidase p
10	254.5	40.4	357	G02937	metcryn alpha - cr
11	253.5	40.2	734	JC4861	fertilin beta - cr
12	252	40.0	616	A55796	fertilin beta cha
13	247.5	39.3	655	JC7850	ecarin precursor -
14	247.5	39.3	660	JC7850	ecarin precursor -
15	246	39.0	416	A17877	disintegrin and me
16	243	38.6	216	JX0265	hemorrhagic protei
17	242.5	38.5	610	JC7530	vascular aggregati
18	240	38.1	789	S28259	androgen-regulate
19	239	37.9	600	J19281	fertilin alpha pre
20	235	37.3	825	S55060	fertilin alpha-ii
21	235	37.3	905	S55059	fertilin alpha-ii
22	233.5	37.1	736	S47645	TMDC II protein - c
23	231	37.0	735	J148101	ADAM 6 protein pre
24	231	36.7	429	A42972	conjugation factor
25	230.5	36.6	732	J15261	testicular metallo
26	228	36.2	209	JX0266	platelet aggregati
27	227	36.0	419	S41607	atrolysin A (EC 3.
28	225	35.8	952	T18900	disintegrin and me
29	223	35.4	549	S48169	metalloproteinase

30	223	35.4	776	2	S28258	androgen-regulated
31	222	35.2	150	2	S60258	metcryn beta - mou
32	222	35.2	473	2	J19283	ADAM 4 protein pre
33	220.5	35.0	713	2	J165253	disintegrin-like t
34	219.5	34.8	777	2	J148100	ADAM 5 protein pre
35	219	34.8	756	2	S47656	TMDC II protein - c
36	217	34.4	1042	2	J26644	hypothetical prote
37	213	33.8	826	2	A60385	monocyte surface a
38	209.5	33.3	823	2	S18968	cytokeratin precurs
39	207	32.9	1239	2	T13809	probable disintegr
40	206.5	32.8	512	2	T137819	probable zinc meta
41	201.5	32.0	544	2	S52477	disintegrin (EC 3.
42	198.5	31.5	491	2	S52920	disintegrin (EC 3.
43	198.5	31.5	748	2	S66129	disintegrin (EC 3.
44	181.5	28.8	83	2	F35982	bican alpha - puff
45	175.5	27.9	83	2	A3156	blisteratin - puff

ALIGNMENTS

RESULT 1
S38539
disintegrin-like metalloproteinase (EC 3.4.24.-), splice form 1 - human
N/Alternate names: ADAM11; MDC
C/Species: Homo sapiens (man)
C/Date: 07-Oct-1994 #sequence_revision 17-Nov-1995 #text_change 26-May-2000
C/Accession: S38539; 152965
R/Emi, M.; Katagiri, T.; Harada, Y.; Saito, H.; Inazawa, J.; Ito, I.; Kasumi, F.; Nakamu
Nature Genet. 5, 151-157, 1993
A/Title: A novel metalloproteinase/disintegrin-like gene at 17q21.3 is somatically rearran
A/Reference number: S38539; MUID:94073190; PMID:8252040
A/Accession: S38539
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-524 <EM1>
A/Cross-references: GB:D17390; NID:G452188; PIDN:BAA04213.1; PID:dl004732; PID:G484255
R/Katagiri, T.; Harada, Y.; Emi, M.; Nakamura, Y.
Cytogenet. Cell Genet. 68, 39-44, 1995
A/Title: Human metalloproteinase/disintegrin-like (MDC) gene: exon-intron organization and
A/Reference number: 152965; MUID:95044425; PMID:7956356
A/Accession: 152965
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 7-225, 'D', 227-524 <KAT>
A/Cross-references: GB:D31872; NID:G505090; PIDN:BAA06671.1; PID:dl007243; PID:G836684
C/Comment: For an alternative splice form, see PIR:165967.
C/Genetics:
A/Genes: GDB:MDC; ADAM11
A/Cross-references: GDB:230267; OMIM:155120
A/Map position: 17q21.3-17q21.3
A/Intons: 28/3; 57/2; 82/3; 105/1; 127/3; 152/3; 176/3; 232/2; 260/3; 291/1; 308/2; 341.
C/Superfamily: disintegrin homology
C/Keywords: alternative splicing; hydrolase; metalloproteinase
F.344-447/Domains: disintegrin homology <DIS>

Query Match 64.2% Score 404.5; DB 2; Length 524;
Best Local Similarity 65.4% Pred. No. 2.3e-25;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

OY 1 PTKLFEPTECGNGVGEAGECDGCFHVECY---GLCCCKSLSGNACSDGPCNNTSCL 57
DB 339 PTKLDPPECGNGVGEAGEEDCCSVGECNAGNCKKCTLTHTDAMCSDDLCCRR--CK 396

OY 58 FQPRGYECRAVNECDITTEYCTGDSGCCPPNHLKQDGYACNQNGRC 104
DB 397 YEPGRVSCRAVNECDIAETCTGDSGCCPPNHLKQDGYACNQNGRC 443

RESULT 2
165967
disintegrin-like metalloproteinase (EC 3.4.24.-), splice form 2 - human
N/Alternate names: ADAM11; MDC

C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 17-Mar-2000 #text_change 11-Jan-2002
C:Accession: 165967, S38539
R:Katagiri, T.; Harada, Y.; Emi, M.; Nakamura, Y.
C:Genet. Cell Genet.: 68, 39-44, 1995
A:Title: Human metalloprotease/disintegrin-like (MDC) gene: exon-intron organization and
A:Reference number: 152965; MUID:95044425; PMID:7955356
A:Accession: 165967
A:Status: translated from GB/EMBL/DBD
A:Molecule type: DNA
A:Residues: 7-670 <Kat>
A:Cross-references: GB:D31872; NID:G505090; PIDN:BA00670.1; PID:G936683
R:Emi, M.; Katagiri, T.; Harada, Y.; Saito, H.; Inazawa, J.; Ito, I.; Kasumi, F.; Nakamura, Y.
Nature Genet.: 5, 151-157, 1993
A:Title: A novel metalloprotease/disintegrin-like gene at 17q21.3 is somatically rearranged
A:Reference number: S38539; MUID:94073190; PMID:8252040
A:Accession: S38539
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-225, 'N', 227-495, 'PQGRAWLPLPCQHLWSSARGFGRQ', <EMI>
A:Cross-references: GB:D17390; NID:G452188; PIDN:BA004213.1; PID:G484255
C:Comment: For an alternative splice form, see PIR:S38539.
C:Genetics:
A:Gene: GDB:MDC, ADAM11
A:Cross-references: GDB:230267; OMIM:155120
A:Map position: 17q21.3-17q21.3
A:Introns: 28/3; 57/2; 82/3; 105/1; 127/3; 152/3; 176/3; 232/2; 260/3; 291/1; 308/2; 341/1
C:Superfamily: disintegrin homology
C:Keywords: alternative splicing; hydrolase; metalloproteinase
C:344-427/Domains: disintegrin homology <DIS>

	Query Match	64.2%	Score 404.5;	DB 2;	Length 670;
	Best Local Similarity	65.4%	Pred. No. 2.7e-25;		
	Matches	70;	Conservative	9;	Mismatches 23; Indels 5; Gaps 2;
Oy	1	PTKLFPEPCNGYVEAGEECDCGFHVECY---	GLCKCKGSLNSGAHCSDPCCNNNSCL	57	
Dd	339	PLKLIDPECGNGFVAGEEBCDCCGSVD	ECSRAGNCCKKCTLTTHAMCSDGLCCR--	CK 396	
Oy	58	FQPRGYECDVAINECDITEYCTGDSGCCPPNHLKHODGACNONGRC	104		
		::			
Dd	397	YEPRGVSCRAVNECDIAETCTGDSGCCPPNHLKLDGYICHDGQR	C 443		

```

RESULT 3
S48160
Metalloproteinase (EC 3.4.24.-) H-I precursor - carpet viper
N:Contains: disintegrin
C:Species: Echis pyramidalis leakeyi
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 21-Jul-2000
C:Accession: S48160
R:Paine, M.J.T.; Moura-Da-Silva, A.M.; Theakston, R.D.G.; Crampton, J.M.
Eur. J. Biochem. 224, 483-488, 1994
A:Title: Cloning of metalloproteinase genes in the carpet viper (Echis pyramidalis leakeyi)
A:Reference number: S48160; MUID:95010025; PMID:7925363
A:Accession: S48160
A:Molecule type: mRNA
A:Residues: 1-617 <P>
A:Cross-references: GB:X78970; NID:G763092; PID:CAAS565.1; PID:G763093
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: hydrolase; metalloproteinase; venom
F.1-18/Domain: signal sequence #status predicted <SIG>
F.19-192/Domain: propeptide #status predicted <PRO>
F.193-617/Product: metalloproteinase H-I #status predicted <MAT>
F.403-485/Domain: disintegrin homology <DIS>
F.337/Active site: GLN #status predicted

```

```

Query March      44.9%; Score 283; DB 2; Length 617;
Best Local Similarity 44.8%; Pred. No. 1.2e-15;
Matches 47; Conservative 17; Mismatches 37; Indels 4; Gaps 2;

OY      2 TRLPEPTCGAGYVAGEGDCGFHVECYGLCK--KSLNAGAHCSGPPCCNNTSCLFQ 59
| : | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Db 399 TDI VSVSGCAGNFVEVGEBCDGGSSNTYCRNPCCATTCKLIRSGQCADBECCN--QGRFR 456

Qy 60 PREGCRDAVNECDITEYCTGDSGQCPNLHKQDSYACNQNGRC 104

Db 457 PARTECRRKIDDCDVEYCTGSGSCPLDFVRNGQDPYQSNNGVC 501

```

RESULT 4
G02390
disintegrin-like metalloproteinase MDC15 (EC 3.4.24.-) - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1995 #sequence_revision 06-Jun-1997 #text_change 31-Dec-2000
C:Accession: G02390; P04263
R:Heinen, B.; Raines, E.W.; Ross, R.
submitted to the EMBL Data Library, January 1996
Reference number: H01157

```

A:Accession: G02390
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-814 <HBR>
A:Cross-references: EMBL:U46005; NID:g1335871; PION:AC51112.1; PID:g1335872
R:McMie, N.; Edwards, T.; Dallas, D.B.; Houston, A.; Stringer, B.; Graham, R.; Russell, B.
Biochem. Biophys. Res. Commun. 230, 335-339, 1997
A:Title: Expression of members of a novel membrane linked metalloproteinase family (ADAM
A:Reference number: PC4263; MUID:97168971; PMID:9016778
A:Accession: PC4263
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-461 <MCK>
A:Experimental source: articular chondrocyte
A:Comment: This protein is a membrane bound protein and involved in cell/cell and cell/m
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: hydrolase; metalloproteinase; zinc
E:420-503/domain: disintegrin homology <DIS>
E:349,352,358/Binding site: zinc (His) #status predicted
E:349/Active site: Glu #status predicted

```
Query March      43.5% Score 274; DB 2; Length 814;  
Beat Local Similarity 48.5%; Pred. No. 7.7e+15;  
Matches 50; Conservative 11; Mismatches 32; Indels 10; Gaps 4  
  
Oy      10 CGGCGVAGEBCEDCGFHVECYGLCKK--GSLSNCAHC-SDQPCCNNTSCLEPQRYEGR 66  
        |||:::|||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      424 CGNNFVEGBECDCGFLDDCVDPCCDSTLCQLRPACASGPCCQN--CQLRPSGMOCR 481  
  
Oy      67 DAVNECDITEXCTGDSGCPENLHKODPYANQNO-----GRC 104  
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|  
Db      482 PTRGDCLDFERCPSGSQCPRPDVSLGDBEPACGAOVCMHGRC 524
```

RESULT 5
S60257
meltrin alpha - mouse
C:Species: Mus musculus (house mouse)
C:Date: 10-Apr-1996 #sequence_revision 19-Apr-1996 #next_change 20-Jun-2000
C:Accession: S60257
R:Yagam-Hiromasa T.; Sato. T.; Kurisaki, T.; Kamiyo, K.; Nabeshima, Y.I.; Fujisawa-Seto
Nature 377, 652-656, 1995
A:Title: A metalloproteinase-disintegrin participating in myoblast fusion.
A:Reference number: S60257; MUID:96026308; PMID:7566181
A:Accession: S60257
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-903 <YMG>
A:Cross-references: EMBL:D50411; NID:g1054586; PIRN:BA08912.1; PIR:g1054587
C:Superfamily: mouse meltrin alpha; disintegrin homology
F:42-503/Domain: disintegrin homology <DIS>
F:349/Active site: Glu #status predicted

Query Match	41.4%	Score 261	DB 2	Length 903
Best Local Similarity	45.1%	Pred. No.	9e-14	
Matches 46	Conservative 12	Mismatches 40	Indels 4	Gaps 2

Qy 5 FEPFECNGVYVGEEDCCDFHVECYGLCK --KSLTSGAHSDSIICNNNSCLFOPG 62
Db 420 FGGRKCGVYVBSBEECDGEPBECTNRCNNATTCUKPDVCAHSHQCCED--CQLKPG 47
Qy 63 YECRDVAIVEDITETCTGDSGQCPRYLHKODGYACNONGRC 104
Db 478 TACGSSNSCLDPEFCTGTAPHRCPRANNVYLDHGPQGVQYIC 519

RESULT 6

metalloprotease (EC 3.4.24.-) (brevilysin) H6, venom - Gloydus halys brevicandus
 N:Contains: disintegrin
 C:Species: Gloydus halys brevicandus
 C:Date: 01-Mar-2002 #sequence_revision 01-Mar-2002 #text_change 21-Apr-2003
 C:Accession: A59414
 R:Iterada, S.
 J. Biochem. 128, 167-173, 2000
 A:Title: Primary Structure and Autoproteolysis of Brevilysin H6 from the Venom of Gloydus
 A:Reference number: A59414
 A:Accession: A59414
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-419 <TER>
 C:Keywords: glycoprotein; hydrolase; metalloprotease; venom; zinc
 F:118-182-187/Disulfide bonds: #status experimental
 F:118-182-187/Disulfide bonds: #status experimental
 F:158-160/Disulfide bonds: (or 158-160) #status experimental
 F:181/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match	40.5%;	Score 255;	DB 2;	Length 419;
Best Local Similarity	41.9%;	Pred. No. 1.7e-13;		
Matches	44;	Conservative	13;	Mismatches 44;
			Indels	4;
			Gaps	2

Qy 2 TXLPEEPGNGVVEAGDEEDCGFHHCEYGLCC--KKGSLSNGAGCSGPPCCNNTSCLFQ 59
Db 206 TDIVSPVVCNELLVEGEBECDCGTPEMNCONECCDAATCTLXKSGSGCCGDCCE--QCKFS 265
Qy 60 PRGECRDVAVNECDITTEYCTGDSGCGPMLHKQDGYACNONGRC 104
Db 264 KSGTECHRESMEPCDPAHCTGGSSSECPAVFHNKQGPCCLDNYGC 308

RESULT 7

Jararagin C precursor - jararaca (fragment)
 N:Alternate names: single chain botrocetin
 N:Contains: disintegrin-like 28k protein; hemorrhagic proteinase (EC 3.4.24.-)
 C:Species: Bothrops jararaca (jararaca)
 C:Date: 20-Feb-1995 #sequence revision 29-Aug-1997 #text_change 09-Jun-2000
 C:Accession: S24789, J02245, A44463, A37958, J02373
 R:Paine, M.J.I. submitted to the EMBL Data Library, August 1992
 A:Reference number: S24789
 A:Accession: S24789
 A:Molecule type: mRNA
 A:Residues: 1-571 <PAI>
 A:Cross-references: EMBL:X68251, NID:G62467, PID:G62468
 B:Usami, Y.; Fujimura, Y.; Mitsu, S.; Shima, H.; Yoshida, E.; Yoshioka, A.; Hirano, K.;
 Biochem. Biophys. Res. Commun. 201, 331-339, 1994
 A:Title: A 28 kDa-protein with disintegrin-like structure (jararagin-C) purified from E
 A:Reference number: J02245, MUID:94256999, PMID:8198592
 A:Accession: J02245
 A:Molecule type: protein
 A:Residues: 360-571 <USA>
 A:Experimental source: venom
 R:Paine, M.J.; Desmond, H.P.; Theakston, R.D.; Crampston, J.M.
 J. Biol. Chem. 267, 22869-22876, 1992
 A:Title: Purification, cloning, and molecular characterization of a high molecular weight
 ily.
 A:Reference number: A44463, MUID:93054601, PMID:1385408
 A:Accession: A44463
 A:Molecule type: mRNA

A:Residues: 1-23 'Q', 25-92, 'G', 94-131, 'G', 133-169, 'Q', 171-571 <RA2>
A:Cross-references: GB:X68251
A:Experimental source: Venom gland
A:Note: sequence inconsistent with the nucleotide translation
A:Note: sequence extracted from NCBI backbone (NCBIP:118104)
R:Fujimura, Y.; Tltani, K.; Usami, Y.; Suzuki, M.; Oyama, R.; Matsui, T.; Fukui, H.; Sug
Biochemistry 30, 1957-1964, 1991
Title: Isolation and chemical characterization of two structurally and functionally di

A:Accession: A37958
A:Molecule type: Protein
A:Residues: 360-372, 'E', 374-378, 'X', 380-384 <FUJ>
A:Note: 361-Val was also found

C:Comment: inhibits collagen- and ADP-induced platelet aggregation
C:Superfamily: mouse meltrin alpha; disintegrin homology
C:Keywords: hydrolase; metalloprotease; venom; zinc
F:360-571/Product: jararagin C #status experimental <MAM>
F:363-444/Domains: disintegrin homology <DIS>
F:295,299,305/Binding site: zinc (HIS) #status predicted
F:296/Active site: Glu #status predicted

Query Match	40.5%;	Score 255;	DB 2;	Length 571;
Best Local Similarity	41.9%;	Pred. No. 2e-13;		
Matches	44;	Conservative	13;	Mismatches 44;
				Indels 4;
				Gaps 2;

QY 2 TKLEPTTECGNGYVAGEECDGCFHYECYGLCC--KKCSLSNGAHCSGDGPPCCNNTSLCFQ 59
| : | | | : | | | | | : : | | | |
Db 358 TDIISPRVCGNELLEVGEECDGCTPENCQNECCDAACTCKLSGSGQCHGDCE--QCKFS 415

QY 60 PRGYECRDVNECDITEYCTGSDSGCCPNLHKQDGYACNQNOSRC 104
 | ||| ::||| :||| :||| :|||
Db 416 KSGTECRASNSECDPAEHCTGQSSECPADVFKHGQPCLDNNGYC 460

RESULT 8

catricollastatin precursor - western diamondback rattlesnake
 C:Species: Crotalus atrox (western diamondback rattlesnake)
 C:Date: 05-Dec-1998 #sequence_revision 05-Dec-1998 #text_change 21-Jul-2000
 C:Accession: S55270
 R:Zhou, Q.; Smith, J.B.; Grossman, M.H.
 Biochem. J. 307, 411-417, 1995
 A:Title: Molecular cloning and expression of catricollastatin, a snake-venom protein from
 A:Reference number: S55264; MUID:95251603; PMID:7733877
 A:Accession: S55270
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-609 <ZHO>
 A:Cross-references: GB:U021003; NID:9710353; PIDN:AACS9672.1; PID:9710354
 C:Superfamily: mouse meltrin alpha; disintegrin homology

Query Match	40.5%;	Score 255;	DB 2;	Length 609;
Best Local Similarity	41.9%;	Pred. No. 2.1e-13;		
Matches 44;	Conservative 13;	Mismatches 44;	Indels 4;	Gaps 2;

QY 2 TKLFEPTECGNGYVAGECCGCGFHVVECYGLCC--KKQSLNSGAHSDSDPCNNNTSLRP 59
Db 396 TDIISPPCGNELLLEVGEBCCDGTRENCQNECCDAATCTLKSGSGQGHEDCEE--GQKFS 453
QY 60 PRGVECDRAVNECDITTEYCTGDSGCCPPMLAKQDGYACNQNQRC 104
Db 454 KSGTECRASMSBECDAEHCCTGQSSSCCPADVPFKNQOPCLDNNGYC 498

RESULT 9

sperm surface protein PH-10 beta chain precursor - guinea pig (fragment)
C.Species: Cavia porcellus (guinea pig)
C.Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jun-2000
Accession: S23403, S25656
R.Label: C.P.; Wolfesberg, T.G.; Turck, C.W.; Myles, D.G.; Primakoff, P.; White, J.M.
Nature 356, 248-252, 1992
Article: A potential fusion peptide and an integrin ligand domain in a protein active in

A:Reference number: S23402; MUID:92204234; PMID:1552944

A:Accession: S23403

A:Molecule type: mRNA

A:Residues: 1-357 <BL01>

A:Cross-references: EMBL:Z11720

A:Accession: S25696

A:Molecule type: protein

A:Residues: 5-8,'X',10-32,67-88,125-129,'X',131-134,'X',136-141,'X',143,154,'X',156-161;

C:Superfamily: mouse meltrin alpha; disintegrin homology

C:Keywords: glycoprotein; transmembrane protein

F:1-4/Domain: signal sequence (fragment) #status predicted <SIG>

F:5-357/Product: sperm surface protein PH-30 beta chain #status experimental <MAT>

F:5-87/Domain: disintegrin homology <DIS>

F:303-323/Domain: transmembrane #status predicted <TMM>

F:78,186,256/Binding site: carbohydrate (Aen) (covalent) #status predicted

Query Match

40.4%; Score 254.5; DB 2; Length 357;

Best Local Similarity 43.1%; Pred. No. 1,6e-13;

Matches 44; Conservative 15; Mismatches 34; Indels 9; Gaps 3;

OY 10 CGNGYVAGEECDCGFHVECYGLCC--KKCSLSNGAGSDGPCNNNTSCLFQPRGYECRD 67

DB 9 CGNNRVEQGEDDCDCSQEGECODTCCDATTCLRLKTSRCAQSPCCN--QCEFTKGEVCRE 66

OY 68 AVNECDITEYCTGDSGQCPNLLHKQGYACNQNQ----GRC 104

DB 67 STDECDDLPEYCNSSGACQEDLYVINGHRCANEWICMNGRC 108

RESULT 10

G02937

fertilin beta - crab-eating macaque

C:Species: Macaca fascicularis (crab-eating macaque)

C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 01-Dec-2000

C:Accession: G02937; S55061

R:Ramarao, C.S.; Wyles, D.G.; White, J.M.; Primakoff, P.

submitted to the EMBL Data Library, August 1995

A:Reference number: G12615

A:Accession: G02937

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-735 <RAM>

A:Cross-references: EMBL:U33959; NID:9998339; PID:9998340

R:Perly, A.C.F.; Gichuhi, P.M.; Jones, R.; Hall, L.

Biochem. J. 307, 843-850, 1995

A:Title: Cloning and analysis of monkey fertilin reveals novel alpha subunit isoforms.

A:Reference number: S55059; MUID:9526013; PMID:7741716

A:Accession: S55061

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-722,'S',724-735 <PER>

A:Cross-references: EMBL:X77653; NID:9794076; PID:CA54733.1; PID:9794077

C:Superfamily: mouse meltrin alpha; disintegrin homology

F:383-466/Domain: disintegrin homology <DIS>

Query Match

40.4%; Score 254.5; DB 2; Length 735;

Best Local Similarity 46.0%; Pred. No. 2,6e-13;

Matches 46; Conservative 11; Mismatches 36; Indels 7; Gaps 3;

OY 10 CGNGYVAGEECDCGFHVECYGL---CC--KKCSLSNGAGSDGPCNNNTSCLFQPRGYE 64

DB 387 CGNAKLEAGEECDCGTCQNCFLGAKCDDTATCRFAGSNCAGPCCEN--CLFMSQERV 444

OY 65 CRDAVNECDITEYCTGDSGQCPNLLHKQGYACNQNQRC 104

DB 445 CRPSFDECDDLPEYCNSTASCPENHFIQTGHPGPNQWVC 484

Search completed: October 21, 2003, 10:11:33
Job time : 30.434 sec

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:02:08 ; Search time 18.3145 Seconds
(without alignments)
267.045 Million call updates/sec

Title: US-09-634-252A-4_COPY_496_599
Perfect score: 630
Sequence: 1 PTKLFPEPCNGYVEAGEE.....CPNHLHKQGYAQNQNGRC 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	404.5	64.2	769	AD11_HUMAN	Q75078 homo sapien
2	404.5	64.2	773	AD11_MOUSE	Q911v4 mus musculu
3	375	59.5	452	AD11_XENLA	Q982z3 xenopus lae
4	364.5	57.9	857	AD22_MOUSE	Q911v6 mus musculu
5	363.5	57.7	906	AD22_HUMAN	Q920k1 homo sapien
6	357.5	56.7	935	AD22_XENLA	Q42596 xenopus lae
7	292	46.3	813	AD33_HUMAN	Q92211 homo sapien
8	274	44.1	816	AD15_RAT	Q947v0 r adam 15 p
9	274	43.5	814	AD15_HUMAN	Q13444 homo sapien
10	269	42.7	797	AD33_MOUSE	Q923w9 mus musculu
11	268	42.5	920	AD19_MOUSE	Q35674 mus musculu
12	267.5	42.5	790	AD30_HUMAN	Q94Kf2 homo sapien
13	263	41.7	815	AD15_MOUSE	Q88839 mus musculu
14	262	41.6	909	AD12_HUMAN	Q41344 homo sapien
15	261	41.4	903	AD12_MOUSE	Q61824 mus musculu
16	259.5	41.2	751	AD02_RABIT	Q28650 oryctolagus
17	258	41.0	776	AD28_MACRA	Q92616 macaca fasc
18	257	40.8	956	AD19_HUMAN	Q92013 homo sapien
19	255	40.5	571	DISJ_BOTJA	P30431 botchops ja
20	254.5	40.4	735	AD02_CAVPO	Q63411 cavia porce
21	254.5	40.4	735	AD02_MACFA	Q28478 macaca fasc
22	254.5	40.4	745	AD02_BOVIN	Q77730 bos taurus
23	253.5	40.2	735	AD02_HUMAN	Q92955 homo sapien
24	252	40.0	616	ECAR_ECHCA	Q90435 echis carin
25	248	39.4	761	AD24_MOUSE	Q91143 mus musculu
26	247.5	39.3	819	AD09_HUMAN	Q13443 homo sapien
27	247	39.2	775	AD28_HUMAN	Q94Kq2 homo sapien
28	246	39.0	416	HRIB_TRIFL	P20152 trimeresunr
29	244.5	38.8	820	AD29_HUMAN	Q94Kf5 homo sapien
30	244	38.7	726	AD20_HUMAN	Q43506 homo sapien
31	242	38.4	722	AD21_HUMAN	Q94Kj8 homo sapien
32	240	38.1	789	AD07_RAT	Q61330 rattus norv
33	235	37.3	788	AD07_MOUSE	Q35327 mus musculu

34	233.5	37.1	697	AD26_MOUSE	Q9158 mus musculu
35	232	36.8	719	AD18_MOUSE	Q9157 mus musculu
36	230	36.5	445	AD18_RAT	P97776 rattus norv
37	223	35.4	754	AD07_HUMAN	Q942u9 homo sapien
38	223	35.4	776	AD07_MACFA	Q28475 macaca fasc
39	221.5	35.2	760	AD25_MOUSE	Q91159 mus musculu
40	220	34.9	729	AD21_MOUSE	Q91176 mus musculu
41	218.5	34.7	746	AD18_MACFA	Q95194 macaca fasc
42	217.5	34.5	737	AD02_RAT	Q63202 rattus norv
43	214.5	34.0	739	AD18_HUMAN	Q94Kq7 homo sapien
44	213	33.8	826	AD08_MOUSE	Q95910 mus musculu
45	211.5	33.6	824	AD08_HUMAN	P78325 homo sapien

ALIGNMENTS

RESULT 1

ID	AD11_HUMAN	STANDARD:	PRT:	769 AA.
AC	Q75078: Q14808; Q14809; Q14810;			
DT	16-OCT-2001 (Rel. 40, Created)			
DT	16-OCT-2001 (Rel. 40, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	ADAM 11 precursor (A disintegrin and metalloproteinase domain 11)			
DE	(Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)			
DE	(MDC)			
GN	ADAM11 OR MDC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_TaxId=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM LONG).			
RC	TISSUE=Brain;			
RX	MEDLINE=96359734; PubMed=9693107;			
RA	Sagane K., Ohya Y., Hasegawa Y., Tanaka I.;			
RT	"Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2 and MDC3: novel human cellular disintegrins highly expressed in the brain.";			
RL	Biochem. J. 334:93-98(1998).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM SHORT).			
RC	TISSUE=Brain, Breast, Ovary, and Testis;			
RX	MEDLINE=95044425; PubMed=7956356;			
RA	Katagiri T., Harada Y., Eml M., Nakamura Y.;			
RT	"A novel metalloproteinase/disintegrin-like gene at 17q21.3 is somatically rearranged in two primary breast cancers.";			
RL	Nat. Genet. 5:151-157(1993).			
RN	[3]			
RP	SEQUENCE OF 106-769 FROM N.A. (ISOFORMS LONG AND SHORT).			
RC	TISSUE=Brain, Breast, Ovary, and Testis;			
RX	MEDLINE=95044425; PubMed=7956356;			
RA	Katagiri T., Harada Y., Eml M., Nakamura Y.;			
RT	"Human metalloproteinase/disintegrin-like (MDC) gene: exon-intron organization and alternative splicing.";			
RL	Cytogenet. Cell Genet. 68:39-44(1995).			
CC	- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON CATALYTIC METALLOPROTEINASE-LIKE PROTEIN.			
CC	- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- ALTERNATIVE PRODUCTS:			
CC	Event=Alternative splicing; Named isoforms=2;			
CC	Name=Long; Synonyms=MDC-769;			
CC	Isoid=O75078-1; Sequence=Displayed;			
CC	Name=Short; Synonyms=MDC-524;			
CC	Isoid=O75078-2; Sequence=VSP_005472; VSP_005473; VSP_005474, VSP_005475;			
CC	- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN BRAIN. SLIGHTLY DETECTED OR NOT AT ALL IN OTHER TISSUES.			
CC	- DOMAIN: A CONSERVED MOTIF (AVN(E/D)CD) WITHIN THE DISINTEGRIN-LIKE DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.			
CC	- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY			

CC SIMILARITY).

CC -1- DISEASE: REARRANGEMENTS OCCUR IN BREAST AND OVARIAN CANCERS WHICH

CC INVOLVE MULTIPLE EXONS AND DISRUPT THE CODING REGION.

CC -1- SIMILARITY: Belongs to peptidase family M12B.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 1 disintegrin domain.

CC -----

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CC -----

DR EMBL, AB009675; BAA3352.1; -

DR EMBL, D17390; BAA0423.1; -

DR EMBL, D1872; BAA0670.1; -

DR PIR, I65967; I65967.

DR HSSP, P18619; 1FVL.

DR MEROPS, M12.976; -

DR Genew, HGNC:189; ADAM11.

DR MIM, 155120; -

DR GO, GO:000586; C:plasma membrane; TAS.

DR GO, GO:0005178; P:integrin binding activity; TAS.

DR GO, GO:0001229; P:integrin-mediated signaling pathway; TAS.

DR InterPro: IPR006586; ADAM cysteine.

DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR006209; EGF-like.

DR InterPro: IPR002870; Pep_M12B_propep.

DR InterPro: IPR001590; RepPolysin.

DR InterPro: IPR006025; Zn_MTPeptidase.

DR Pfam: PF00200; disintegrin; 1.

DR Pfam: PF01562; Pep_M12B_propep; 1.

DR Pfam: PF01421; RepPolysin; 1.

DR PRINTS; PR00289; DISINTEGRIN.

DR ProDom; PD000664; Disintegrin; 1.

DR SMART; SMO0050; DISIN; 1.

DR SMART; SMO0050; DISIN; 1.

DR PROSITE; PSS0215; ADAM MEPRO; 1.

DR PROSITE; PSS0427; DISINTEGRIN_1; FALSE_NEG.

DR PROSITE; PSS0214; DISINTEGRIN_2; 1.

DR PROSITE; PSS0022; EGF_1; 1.

DR PROSITE; PSS0186; EGF_2; FALSE_NEG.

DR PROSITE; PSS0142; ZINC_PROTEASE; FALSE_NEG.

KM Signal; Glycoprotein; Transmembrane; EGF-like domain;

KM Alternative splicing.

FT SIGNAL 1 23

FT PROPEP 24 225

FT CHAIN 226 769

FT DOMAIN 226 734

FT TRANSMEM 735 755

FT DOMAIN 756 769

FT DOMAIN 226 438

FT DOMAIN 444 531

FT DOMAIN 532 676

FT DOMAIN 677 709

FT DISULFID 349 433

FT DISULFID 503 516

FT DISULFID 677 692

FT DISULFID 677 698

FT DISULFID 700 709

FT CARBOHYD 96 163

FT CARBOHYD 163 163

FT CARBOHYD 605 605

FT CARBOHYD 673 673

FT VARSPLIC 1 99

FT VARSPLIC 100 104

FT VARSPLIC 595 623

FT VARSPLIC 595 623

FT FT /FTid=VSP_005474.

FT VARSPLIC 624 769 Missing (in isoform Short).

FT CONFLICT 106 106 /FTid=VSP_005475.

FT CONFLICT 325 325 Q -> N (IN REF. 1).

FT CONFLICT 325 325 D -> N (IN REF. 2).

SQ SEQUENCE 769 AA; 83409 MW; 5989C46786DDP6B6 CRC64;

Query Match 64.2%; Score 404.5; DB 1; Length 769;

Best Local Similarity 65.4%; Pred. No. 4.7e-27;

Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

QY 1 PTKLEPTECGNGVYAGEECDCGFHYECY---GLCKKCSLSNGAHCSGSPCCNNTSCL 57

DB 438 PLKLLDPCECGNGFVAGEECDCGSGVQCSRAGNCKKCTLTHDAMCSDSGLCCR--CK 495

QY 58 FOPRGYECRDVAVNEDITEYCTGSGGCGPPNHLKODGACACNONGRC 104

DB 496 YEPRGVSCRAVNECDIAETCTGDSGCPNHLKIDGYCDHEQGR 542

RESULT 2

ID AD11_MOUSE STANDARD; PRT; 773 AA.

AC Q9RIV4;

DT 16-OCT-2001 (Rel. 40; Created)

DT 16-OCT-2001 (Rel. 40; Last sequence update)

DT 16-OCT-2001 (Rel. 40; Last annotation update)

DE ADAM 11 precursor (A disintegrin and metalloproteinase domain 1)

DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)

DE (MDC).

GN ADAM11 OR MDC.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_Taxid=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RC MEDLINE=99365303; PubMed=10433968;

RA Sagane K., Yamazaki K., Mizui Y., Tanaka I.;

RT "Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23.";

RL Gene 236:79-86(1999).

CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON

CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.

CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. WEAKLY

CC DETECTED IN THE HEART, LIVER AND TESTIS.

CC -1- DOMAIN: A CONSERVED MOTIF [AVN(E/D)CD] WITHIN THE DISINTEGRIN-LIKE

CC DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.

CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY

CC SIMILARITY).

CC -1- SIMILARITY: Belongs to peptidase family M12B.

CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 1 disintegrin domain.

CC -----

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CC -----

DR EMBL, AB009675; BAA8384.1; -

DR HSSP, P18619; 1FVL.

DR MEROPS, M12.976; -

DR MGD; MGI:1098667; Adam11.

DR InterPro: IPR006586; ADAM cysteine.

DR InterPro: IPR001762; Disintegrin.

DR InterPro: IPR006209; EGF-like.

DR InterPro: IPR002870; Pep_M12B_propep.

DR InterPro: IPR001590; RepPolysin.

DR InterPro: IPR006025; Zn_MTPeptidase.

DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Peg_M12B_propep; 1.
DR Pfam; PF01421; Repolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR Pfam; PF000664; disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain.
FT SIGNAL 1 24
FT PROPEP 25 229
FT CHAIN 230 773
FT DOMAIN 230 738
FT TRANSMEM 739 759
FT DOMAIN 760 773
FT DOMAIN 230 442
FT DOMAIN 448 535
FT DOMAIN 536 680
FT DOMAIN 681 713
FT DISULFID 353 437
FT DISULFID 507 520
FT DISULFID 681 696
FT DISULFID 690 702
FT DISULFID 704 713
FT CARBOHYD 100 100
FT CARBOHYD 167 167
FT CARBOHYD 609 609
FT CARBOHYD 677 677
SQ SEQUENCE 773 AA; 84134 MW; 9ABAI25FB3F743DD CRC64;

Query Match 64.2%; Score 404.5; DB 1; Length 773;
Best Local Similarity 65.4%; Pred. No. 4.7e-27;
Matches 70; Conservative 9; Mismatches 23; Indels 5; Gaps 2;

OY 1 PTKLPEFGCGNGVGEAGEGDCGPFHVC---GLCKCKKSLNSGACGSDGPCNNNTSC 57
DB 442 PLKLLDPPSCNGGFIIEGECDCGSPACCKNSRAGNCKCKCTTSHDMWCSGLCCR--CG 499
OY 58 FQPRGYECRDVAVECDITEYCTGDSGCGCPNHLKOGYACNONGRC 104
DB 500 YEPGVSCRAVNECDIETCTGDSGCGCPNHLKIDGYCHGQRC 546

RESULT 3
AD11_XENLA STANDARD; PRT; 452 AA.
AC OPR523;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADAM 11 (A disintegrin and metalloproteinase domain 11)
DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein)
DE (MDC) (Metalloproteinase-disintegrin MDC11a) (MDC11.1) (Fragment).
CN ADAM11 OR MDC11A.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC Xenodidae; Xenopus.
NCBI_TaxID=8355;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=99102794; PubMed=9882486;
RA Cai H., Kraetzschmar J., Alfandari D., Hunnicutt G., Blöbel C.P.;
RT "Neural crest-specific and general expression of distinct
RT metalloproteinase-disintegrins in early Xenopus laevis development";
RL Dev. Biol. 204:508-524(1998).
CC -!- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON

CC CATALYTIC METALLOPROTEINASE-LIKE PROTEIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: DETECTED IN TESTIS AND BARELY EXPRESSED IN
CC HEART AND MUSCLE. NOT DETECTABLE IN LIVER.
CC -!- DEVELOPMENTAL STAGE: COULD NOT BE DETECTED IN EMBRYOS UNTIL
CC NEURULATION. IN DEVELOPING EMBRYOS, THE EXPRESSION IS RESTRICTED
CC TO NEURAL CREST DERIVATIVES.
CC -!- DOMAIN: A CONSERVED MOTIF (AVN(E/D)CD) WITHIN THE DISINTEGRIN-LIKE
CC DOMAIN COULD BE INVOLVED IN THE BINDING TO THE INTEGRIN RECEPTOR.
CC -!- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -!- SIMILARITY: Belongs to peptidase family M12B.
CC -!- SIMILARITY: Contains 1 EGF-like domain.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
CC -!- SIMILARITY: Contains 1 disintegrin domain.
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CC or send an email to license@isb-sib.ch).

DR EMBL; AF032384; AAC61848.1; -!
DR HSSP; P18619; 1FV1.
DR MEROPS; M12. UNB; -!
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR001590; Repolysin.
DR InterPro; IPR006025; Zn MTpeptidase.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01421; Repolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR Pfam; PF000664; disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
KW Glycoprotein; Transmembrane; EGF-like domain.
FT NON_TER 1 1
FT DOMAIN <1 417
FT TRANSMEM 418 438
FT DOMAIN 439 452
FT DOMAIN <1 120
FT DOMAIN 126 214
FT DOMAIN 215 359
FT DOMAIN 360 416
FT DISULFID 31 115
FT DISULFID 186 199
FT DISULFID 360 375
FT DISULFID 369 381
FT DISULFID 383 392
FT CARBOHYD 149 149
FT CARBOHYD 288 288
FT CARBOHYD 356 356
SQ SEQUENCE 452 AA; 48577 MW; D11F66C24CCD6847 CRC64;

Query Match 59.5%; Score 375; DB 1; Length 452;
Best Local Similarity 58.3%; Pred. No. 9e-25;
Matches 63; Conservative 12; Mismatches 27; Indels 6; Gaps 2;

OY 1 PTKLPEFGCGNGVGEAGEGDCGPFHVC---GLCKCKKSLNSGACGSDGPCNNNTSC 56
DB 120 PLKLLDPPSCNGGFIIEGECDCGSPACCKNSRAGNCKCKCTTSHDMWCSGLCCR--CG 177
OY 57 LFQPRGYECRDVAVECDITEYCTGDSGCGCPNHLKOGYACNONGRC 104

Db 178 KKEPRGTVCRESLNECDVBEACPDSDSACAPNLHKQDGYFCNDEQRC 225

RESULT 4

AD22_MOUSE STANDARD; PRT; 857 AA.
AC Q9R1V6; Q9R1V5; 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22).
GN ADAM22.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN (1)
RP SEQUENCE FROM N.A. (ISOFORMS ALPHA AND BETA).
RC TISSUE=Brain;
RX MEDLINE=99365303; PubMed=10433968;
RA "Sagane K., Yamazaki K., Mizui Y., Tanaka I.;
RL Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23.";
RL Gene 236:79-86 (1999).
CC - FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC - ALTERNATIVE PRODUCTS: Type I membrane protein.
CC Event=Alternative splicing; Named isoforms=2;
CC Name=Alpha;
CC IsoId=Q9R1V6-1; Sequence=Displayed;
CC Name=Beta;
CC IsoId=Q9R1V6-2; Sequence=VSP_005485;
CC - TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN THE BRAIN.
CC - PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC - SIMILARITY: Belongs to peptidase family M12B.
CC - SIMILARITY: Contains 1 EGF-like domain.
CC - SIMILARITY: Contains 1 disintegrin domain.
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CC
CC EMBL; AB009674; BAA83382.1; -
CC EMBL; AB009674; BAA83383.1; -
CC HSSP; P18619; 1FVL.
CC MGD; MGI:1340046; Adam22.
DR InterPro: IPR006586; ADAM_cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR002870; Pep_M12B_propep.
DR InterPro: IPR001590; Reptolysin.
DR InterPro: IPR006025; Zn_MTPptidse.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reptolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; D1SIN; 1.
DR PROSITE; PS50215; ADAM_MEPPO; 1.
DR PROSITE; PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE; PS00024; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
KW Signal; Glycoprotein; Transmembrane; EGF-like domain;
KW Alternative splicing.

FT SIGNAL 1 23
FT PROPEP 24 223
FT CHAIN 224 857
FT DOMAIN 24 734
FT TRANSMEM 735 755
FT DOMAIN 756 857
FT DOMAIN 224 436
FT DOMAIN 442 529
FT DOMAIN 533 666
FT DOMAIN 673 710
FT DISULFID 347 431
FT DISULFID 501 514
FT DISULFID 677 692
FT DISULFID 686 698
FT DISULFID 700 709
FT CARBOHYD 517 163
FT CARBOHYD 517 517
FT CARBOHYD 632 632
FT CARBOHYD 673 673
FT VARSPLIC 766 801
SQ SEQUENCE 857 AA; 94740 MW; CB88F87000208E09 CRC64;
Query Match 57.9%; Score 364.5; DB 1; Length 857;
Best Local Similarity 57.0%; Pred. No. 1.1e-23;
Matches 61; Conservative 14; Mismatches 27; Indels 5; Gaps 2;
QY 1 PTKLEPFEPCNGVYAEEDCGFHVEY---GLCKKCSLSNAGHSDDPCNNITGCL 57
DB 436 PSKLLDPEPCNGVYAEEDCGFHVEY---GLCKKCSLSNAGHSDDPCNNITGCL 57
QY 58 FQPRGYECRDVAVNECDITEYCTGDSGQCPNHLKQDGYACNONGRC 104
DB 436 FQPLCTVGRVAVNDCDITEYCTGDSGQCPNHLKQDGYACNONGRC 104
Db 494 FQPLCTVGRVAVNDCDITEYCTGDSGQCPNHLKQDGYACNONGRC 104
RESULT 5
AD22_HUMAN STANDARD; PRT; 906 AA.
ID AD22_HUMAN
AC Q9P0K1; Q75075; Q75076; Q9P0K2; Q9U1A1; Q9UUK2;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)
DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein
DE 2) (Metalloproteinase-disintegrin ADAM22-3).
GN ADAM22 OR MDC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RX MEDLINE=20504287; PubMed=11050470;
RA Harada T., Nishie A., Torigoe K., Ikezaki K., Shono T., Maehara Y.,
RA Kuwano M., Wada M.;
RT "The specific expression of three novel splice variant forms of human
RT metalloproteinase-like disintegrin-like cysteine-rich protein 2 gene
RT in brain tissues and gliomas."
RL Jpn. J. Cancer Res. 91:1001-1006 (2000).
RL [2]
RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
RC TISSUE=Brain;
RX MEDLINE=98359734; PubMed=9693107;
RX Sagane K., Ohya Y., Hasegawa Y., Tanaka I.;
RA "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
RT and MDC3: novel human cellular disintegrins highly expressed in the
RT brain";
RL Biochem. J. 334:93-98 (1998).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM 5).
RC TISSUE=Brain;
KW Wada M., Torigoe K., Harada T., Kuwano M.;

RT "Isolation and tissue specific expression of novel ADAM family from
RT 7q21.1 region."
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 40-906 FROM N.A. (ISOFORM 1).
RC TISSUE=Cerebellum;
RA MEDLINE=99453762; Pubmed=10524237;
RX Polidexter K., Nelson N., Dubose R.F., Black R.A., Cerretti D.P.;
RT "The identification of seven metalloproteinase-disintegrin (ADAM)
RL Gene from genomic libraries."
CC Gene 237.61-70(1999).
CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=5;
CC Name=1; Synonyms=Dsillon;
CC IsoId=Q9P0K1-1; Sequence=displayed;
CC Name=2; Synonyms=Delta;
CC IsoId=Q9P0K1-2; Sequence=VSP_005482, VSP_005484;
CC Name=3; Synonyms=Alpha;
CC IsoId=Q9P0K1-3; Sequence=VSP_005483;
CC Name=4; Synonyms=Beta;
CC IsoId=Q9P0K1-4; Sequence=VSP_005482, VSP_005483;
CC Name=5;
CC IsoId=Q9P0K1-5; Sequence=VSP_005482;
CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. DETECTED SLIGHTLY
CC OR NOT AT ALL IN OTHER TISSUES.
CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
CC SIMILARITY).
CC -1- SIMILARITY: Belongs to peptidase family M12B.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -----
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CC -----
DR EMBL; AF155382; AAF73289.1; -
DR EMBL; AF155381; AAF73288.1; -
DR EMBL; AB009671; BAA32349.1; -
DR EMBL; AB009671; BAA32350.1; -
DR EMBL; AF073291; AAF22476.2; -
DR EMBL; AF158637; AAD55251.1; -
DR HSSP; P18619; 1FVL.
DR MEROPS; M12.978; -
DR Genew; HGNC:201; ADAM22.
DR MTM; 603709; -
DR GO; GO:0016021; C:integral to membrane; NAS.
DR GO; GO:0005178; F:integrin binding activity; NAS.
DR GO; GO:0007162; P:negative regulation of cell adhesion; NAS.
DR InterPro; IPR006586; ADAM cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR002870; Pep_M12B_propep.
DR InterPro; IPR001590; Reptolysin.
DR InterPro; IPR006025; Zn_MTpeptidse.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Pep_M12B_propep; 1.
DR Pfam; PF01421; Reptolysin; 1.
DR PRINTS; PR00289; DISINTEGRIN.
DR Prodom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00650; DISIN; 1.
DR PROSITE; PS00425; ADAM_MERO; 1.
DR PROSITE; PS00427; DISINTEGRIN; 1; FALSE_NEG.
DR PROSITE; PS00214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.

DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.
KM Signal; Glycoprotein; Transmembrane; EGF-like domain;
RN Alternative splicing.
FT SIGNAL 1 25
FT PROPEP 26 222
FT CHAIN 223 906
FT DOMAIN 223 736
FT TRANSEM 737 757
FT DOMAIN 758 906
FT DOMAIN 223 438
FT DOMAIN 444 531
FT DOMAIN 532 678
FT DOMAIN 675 712
FT DISULFID 349 433
FT DISULFID 503 516
FT DISULFID 679 694
FT DISULFID 688 700
FT DISULFID 702 711
FT CARBOHYD 175 175
FT CARBOHYD 519 519
FT CARBOHYD 634 634
FT CARBOHYD 675 675
FT VARSPPLIC 768 803
FT
FT VARSPPLIC 860 906
FT
FT VARSPPLIC 859 859
FT
FT CONFLICT 81 81
SQ SEQUENCE 906 AA; 100432 MW; 265ECCD0FA6C088B CRC64;

Query Match 57.7%; Score 363.5; DB 1; Length 906;
Best Local Similarity 57.0%; Pred. No. 1,4e-23;
Matches 61; Conservative 14; Mismatches 27; Indels 5; Gaps 2;

QY 1 PTKLFEPTGCGNGVGEAGEGDCGPHVECY---GLCKKCSLSNGAHCSDGPCNNNTSCL 57
Db 438 PSKLLDPPECGNGFIETGSECDGCTRAECVLEGAECCKKTLVLDSCSGLCK--KCK 495
QY 58 FQPRGVECRDAVNECDITTEYCTGDSGQCPNHLKODGYACNOGRC 104
Db 496 FQPMGTGCREAVNVDCDIRTCGNSGSCAPNHHKMDGVCSDGVQIC 542

RESULT 6
AD22_XENLA STANDARD; PRT; 935 AA.
ID AD22_XENLA
AC 042596;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)
DE (Metalloproteinase-disintegrin MDC11b) (MDC11.2).
GN ADAM22 OR-MDC11B.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=99102794; Pubmed=9882486;
RX Cai H., Kraetzschmar J., Alfandari D., Hunnicutt G., Blobel C.P.;
RT "Neural crest-specific and general expression of distinct
RT metalloproteinase-disintegrins in early Xenopus laevis development."
RL Dev. Biol. 204:508-524(1998).
RN [2]
RP SEQUENCE OF 464-511 FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=97349132; Pubmed=9205136;

RA Shilling F.M., Kraetzschmar J., Cai H., Weskamp G., Gayko U.,
 RA Lebow J., Myles D.G., Nucitelli R., Blobel C.P.;
 RT "Identification of metalloprotease/diintegrins in *Xenopus laevis*
 RT testis with a potential role in fertilization.",
 RU Dev. Biol. 186:155-164(1997).
 CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
 CC CATALYTIC METALLOPROTEASE-LIKE PROTEIN (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: LOW LEVELS IN ADULT TISSUES. NOT DETECTED IN
 CC DEVELOPING EMBRYOS.
 CC -1- PFM: THE PRECURSOR IS CLEAVED BY A PURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL, AF032383; AAC61847.1; -
 CC EMBL, U78188; AAB87148.1; -
 CC HSSP; P17347; 2ECH.
 CC DR MEROPS; M12_UBP; -
 CC DR InterPro; IPR006586; ADAM cysteine.
 CC DR InterPro; IPR001762; Disintegrin.
 CC DR InterPro; IPR006209; EGF-like.
 CC DR InterPro; IPR006210; IEGF.
 CC DR InterPro; IPR002870; Pep_M12B_propep.
 CC DR InterPro; IPR001590; Reprolysin.
 CC DR InterPro; IPR006025; Zn_MTPeptide.
 CC DR Pfam; PF00200; disintegrin; 1.
 CC DR Pfam; PF01562; Pep_M12B_propep; 1.
 CC DR Pfam; PF01421; Reprolysin; 1.
 CC DR ProDom; PD000664; Disintegrin; 1.
 CC DR SMART; SM00608; ACR; 1.
 CC DR SMART; SM00608; DISIN; 1.
 CC DR SMART; SM00181; EGF; 1.
 CC DR PROSITE; PS50215; ADAM_MEROP; 1.
 CC DR PROSITE; PS50427; DISINTEGRIN_1; 1.
 CC DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 CC DR PROSITE; PS00022; EGF_1; 1.
 CC DR PROSITE; PS01186; EGF_2; FALSE NEG.
 CC DR PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
 CC DR PROSITE; PS00142; ZINC_PROTEASE; FALSE NEG.
 CC Signal; Glycoprotein; Transmembrane; EGF-like domain.
 CC KW SIGNAL 1 24
 CC FT PROPEP 25 227
 CC FT CHAIN 228 935
 CC FT DOMAIN 228 736
 CC FT TRANSMEM 727 757
 CC FT DOMAIN 728 935
 CC FT DOMAIN 228 440
 CC FT DOMAIN 446 533
 CC FT DOMAIN 536 670
 CC FT DOMAIN 677 713
 CC FT DISULFID 351 435
 CC FT DISULFID 505 518
 CC FT DISULFID 681 695
 CC FT DISULFID 689 701
 CC FT DISULFID 703 712
 CC FT CARBOHYD 167 167
 CC FT CARBOHYD 210 210
 CC FT CARBOHYD 521 521
 CC FT CARBOHYD 609 609
 CC FT CARBOHYD 636 636
 CC FT CARBOHYD 677 677
 CC SEQUENCE 935 AA, 104161 MW, 7787ADCC5C77C90 CXC64;
 Query Match 56.7%; Score 357.5; DB 1; Length 935;

Best Local Similarity 57.0%; Pred. No. 4,66-23;
 Matches 61; Conservative 13; Mismatches 28; Indels 5; Gaps 2;
 Oy 1 PTKLPEPTCCNGVVEAGEEDCGFHVET---GLCKCKGLSGAHSDPCCNNISCL 57
 Db 440 PLKLDPECCNGVVEAGEEDCGFHVET---GLCKCKGLSGAHSDPCCNNISCL 57
 Oy 58 FQPGYECRDVAVNECDITVEYCTGSDGCPPLVLRKQDGYACQNGRC 104
 Db 498 FNPKEMLCREAVNCDIPETCTGNTSCCPANIHRLDGYSCSMQGLC 544
 RESULT 7
 AD33 HUMAN STANDARD; PRT; 813 AA.
 ID AD33 HUMAN
 AC 098RT1;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DE 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM 33 precursor (EC 3.4.24.-) (A disintegrin and metalloprotease
 DE domain 33).
 GN ADAM33.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 ON NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Testis;
 RX MEDLINE=21674006; PubMed=11814695;
 RA Yoshinaka T., Nishii K., Yamada K., Sawada H., Nishiwaki E., Smith K.,
 RA Yoshino K., Ishiguro H., Higashiyama S.;
 RT "Identification and characterization of novel mouse and human ADAM33
 RT with potential metalloprotease activity.",
 RL Gene 282:227-236(2002).
 RN [2]
 RP SEQUENCE OF 86-813 FROM N.A.
 RX MEDLINE=21638749; PubMed=11780052;
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,
 RA Jones M., Stavrides G., Almeida J.P., Babidge A.K., Baggley C.L.,
 RA Bailey J., Barlow K.F., Bates K.N., Bead L.M., Beare D.M.,
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
 RA Buck D., Buttrill W.D., Butler A.P., Carder C., Carter N.P.,
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
 RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Cobby N.R.,
 RA Coulson A., Coville G.J., Deadman R., Dhami P.D., Dunn M.R.,
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,
 RA Lehaeslajho M.H., Leverisha M.A., Lloyd C., Lloyd D.M., Lovell J.D.,
 RA Marsh V.L., Martin S.L., McComachie L.J., McElay K., McMurtry A.A.,
 RA Milne S.A., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,
 RA Phillimore B.J.C.T., Prathalingam S.R., Plumb R.W., Ramsay H.,
 RA Rice C.M., Ross M.T., Scott C.E., Sehra H.K., Shownkeen R., Sims S.,
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,
 RA Swann R.M., Sycanore N., Taylor R., Tee L., Thomas D.W., Thorpe A.,
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,
 RA Wilming L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,
 RA Rogers J.;
 RT "The DNA sequence and comparative analysis of human chromosome 20.",
 RL Nature 414:865-871(2001).
 CC -1- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9B211-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q9B211-2; Sequence=VSP_005495;

CC -1- TISSUE SPECIFICITY: Expressed in all tissues, except: liver, with
 CC high expression in placenta, lung, spleen and veins.
 CC -1- PM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC or send an email to license@ebi-emb.ch).
 CC -----
 CC EMBL: AB055891; BAB83092.1; -
 CC EMBL: AL356755; CAC16509.2; -
 CC HSSP: P18619; 1FVL.
 CC MEROPS: M12.239; -
 CC Genew: HGNC:15478; ADAM33.
 CC MIM: 607114; -
 CC GO: GO:0016021; C:integral to membrane; NAS.
 CC GO: GO:0004222; F:metalloendopeptidase activity; NAS.
 CC GO: GO:0008270; F:zinc ion binding activity; NAS.
 CC GO: GO:0006508; P:proteolysis and peptidolysis; NAS.
 CC GO: GO:0042127; P:regulation of cell proliferation; ISS.
 CC GO: GO:0042035; P:regulation of cytokine biosynthesis; ISS.
 CC InterPro: IPR006586; ADAM_cysteine.
 CC InterPro: IPR001762; Disintegrin.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR001818; Matrxin.
 CC InterPro: IPR002870; Pep_M12B_propep.
 CC InterPro: IPR001590; Retriolysin.
 CC InterPro: IPR006925; Zn_M12B_pep.
 CC Pfam: PF00200; disintegrin.1.
 CC Pfam: PF01562; Pep_M12B_propep.1.
 CC Pfam: PF01421; Retriolysin.1.
 CC PRINTS: PR00289; DISINTEGRIN.
 CC PRODOM: PD000664; disintegrin.1.
 CC SMART: SM00608; ACR.1.
 CC SMART: SM00500; DISIN.1.
 CC PROSITE: PS50215; ADAM_MEPPO.1.
 CC PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 CC PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
 CC PROSITE: PS50214; DISINTEGRIN_2; 1.
 CC PROSITE: PS00022; EGF_1; FALSE_NEG.
 CC PROSITE: PS01186; EGF_2; 1.
 CC PROSITE: PS00142; ZINC_PROTEASE; 1.
 CC Hydrolase: Metalloprotease; zinc; Signal; Glycoprotein; Zymogen;
 CC Transmembrane; EGF-like domain; Alternative splicing.
 CC SIGNAL 1 29
 CC PROPEP 30 203
 CC CHAIN 204 813
 CC DOMAIN 30 701
 CC TRANSMEM 702 722
 CC DOMAIN 723 813
 CC DOMAIN 204 409
 CC DOMAIN 417 502
 CC DOMAIN 503 648
 CC DOMAIN 649 681
 CC METALLOPROTEASE 681
 CC DISINTEGRIN-LIKE 681
 CC CYS-RICH 681
 CC EGF-LIKE 681
 CC CYSTEINE SWITCH (POTENTIAL) 681
 CC ZINC (CATALYTIC) (BY SIMILARITY) 681
 CC ZINC (CATALYTIC) (BY SIMILARITY) 681
 CC ACT SITE 346 349
 CC METAL 349 349
 CC METAL 355 355
 CC DISULFID 320 404
 CC DISULFID 360 388
 CC DISULFID 475 488
 CC DISULFID 653 663
 CC DISULFID 657 669
 CC DISULFID 671 680
 CC CARBOHYD 109 109
 CC N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 145 145 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 276 276 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 448 448 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT VARSPIC 636 661 Missing (in isoform 2).
 FT SEQUENCE 813 AA; 8773 MW; 90713A956805569 CRC64;
 SO
 Query Match 46.3%; Score 292; DB 1; Length 813;
 Best Local Similarity 51.0%; Pred. No. 1,2e-17;
 Matches 51; Conservative 11; Mismatches 34; Indels 4; Gaps 2;
 Oy 7 PTEGNGVYDAGEECDCGFHVECYGLCC--KCSLSGACMSDGPCCNNTSCLFPQSGYE 64
 Db 417 PALCGNFEVAGEECDCGPGCECRDLCCFAHNCGLRPGACCAHGDCC--VRCLLKPAAGAL 474
 Oy 65 CRDAVNECDITEVCTSGDSCGCPRLHKQDPAACNONGRC 104
 Db 475 CRQMGDCDLPFETGTSRHCPDVYLLDGPSCARGSGYC 514
 RESULT 8
 AD15_RAT STANDARD; PRT; 816 AA.
 ID AD15_RAT
 AC Q9QYV0;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
 DE domain 15) (Metalloprotease-like, disintegrin-like, and cysteine-
 DE rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
 DE (Metargidin) (CRII-7).
 DE ADAM15 OR MDC15.
 GN Rattus norvegicus (Rat).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId:10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Sciatic nerve;
 RX MEDLINE=20556183; PubMed=11102971;
 RA Bosse F., Petzold G., Greiner-Petters R., Pipplars U., Gillen C.,
 RA Mueller H.-W.;
 RT "Cellular localization of the disintegrin CRII-7/WDC15 mRNA in rat
 RT PNS and CNS and regulated expression in postnatal development and
 RT after nerve injury";
 RL Glia 32:313-327(2000).
 CC -1- FUNCTION: May be involved in cell-surface proteolysis, cell
 CC adhesion or intracellular protein maturation.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (Potential).
 CC -1- SUBUNIT: Interacts with ITGA5-ITGB3 (vitronectin receptor),
 CC PACSIN3 and SNX. PACSIN3 and SNX9 preferentially bind the
 CC precursor but not the processed form of ADAM15, suggesting that
 CC the interaction occurs in a secretory pathway compartment prior to
 CC the medial Golgi (By similarity). Interacts specifically with Src
 CC family protein-tyrosine kinases (PTKs) (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: PREDOMINANTLY EXPRESSED IN BRAIN, SPINAL CORD,
 CC SCIATIC NERVE AND LUNG. EXPRESSED AT LOWER LEVELS IN ALL OTHER
 CC TISSUES. IN THE PERIPHERAL NERVOUS SYSTEM, EXPRESSED PREDOMINANTLY
 CC BY SCHWANN CELLS. IN THE CENTRAL NERVOUS SYSTEM, PREFERENTIALLY
 CC EXPRESSED BY NEURONAL CELLS.
 CC -1- INDUCTION: IN RESPONSE TO SCIATIC NERVE INJURY.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
 CC SORTING NEXIN 9 (BY SIMILARITY).
 CC -1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA-V-BETA3 (BY
 CC SIMILARITY).
 CC -1- PTM: Phosphorylation increases association with PTKs (By
 CC similarity).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.

CC -1- SIMILARITY: Contains 1 disintegrin domain.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ251198; CAB61762.1; -.
DR HSRP: P17494; IKST.
DR MEROPS: M12.215; -.
DR InterPro: IPR006586; ADAM cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006209; EGF like.
DR InterPro: IPR001818; Matrxin.
DR InterPro: IPR002870; Pep_M12B_propep.
DR InterPro: IPR001590; Reptolysin.
DR InterPro: IPR006025; Zn_MTPeptidase.
DR Pfam: PF00200; disintegrin; 1.
DR Pfam: PF01562; Pep_M12B_propep; 1.
DR Pfam: PF01421; Reptolysin; 1.
DR ProDom: PD000664; Disintegrin; 1.
DR SMART: SMO0608; ACR; 1.
DR SMART: SMO0050; DISIN; 1.
DR PROSITE: PS00215; ADAM_MEROP; 1.
DR PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
DR PROSITE: PS00214; DISINTEGRIN_2; 1.
DR PROSITE: PS00022; EGF_1; FALSE_NEG.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.
DR Hydrolase: Metalloprotease; Zinc; Signal: Glycoprotein; Zymogen;
KW Transmembrane; EGF-like domain; SH3-binding; Phosphorylation.
FT SIGNAL 1 17
FT PROPEP 18 208
FT CHAIN 209 698
FT DOMAIN 209 698
FT TRANSMEM 699 719
FT DOMAIN 720 816
FT DOMAIN 209 416
FT DOMAIN 423 510
FT DOMAIN 511 658
FT DOMAIN 659 687
FT DOMAIN 700 713
FT SITE 768 774
FT SITE 803 809
FT SITE 180 180
FT METLA 350 350
FT ACT SITE 351 351
FT METLA 351 351
FT METLA 354 354
FT METLA 360 360
FT METLA 360 360
FT DISULFID 325 411
FT DISULFID 482 495
FT DISULFID 659 669
FT DISULFID 663 677
FT DISULFID 677 686
FT MOD_RES 717 717
FT MOD_RES 737 737
FT CARBOHYD 57 57
FT CARBOHYD 239 239
FT CARBOHYD 391 391
FT CARBOHYD 394 394
FT CARBOHYD 608 608
FT CARBOHYD 613 613
SQ SEQUENCE 816 AA; 88051 NM; B9D2CEB023266FC27 CRC64;
Query Match 44.1%; Score 278; DB 1; Length 816;
Best Local Similarity 48.5%; Pred. No. 18e-16;
Matches 50; Conservative 12; Mismatches 31; Indels 10; Gaps 4;
OY 10 CGNGVAGEECDCGFHVCYGLCK--KCSLSNGAHC--SDGPCNNTSCLFQPGYECR 66

DB 426 CGNMFVDEFGCDGCFPECTDPCDYPFTCOLRGAQACASGPCCN--CTLGPAGWCCR 483
OY 67 DANNEDCTEYCTGDSGCGCPNHLKQDGYACNQG-----CRC 104
DB 484 LPTDDCDLPEFLGDSGQCPDRLRGDEPCASGAVCMHGRG 526
RESULT 9
AD15_HUMAN
ID AD15_HUMAN STANDARD; PRT; 814 AA.
AC Q13444; Q13493; Q96C78;
DT 16-OCT-2001 (Rel. 40, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADAM 15 precursor (EC 3.4.24.-) (A disintegrin and metalloproteinase
DE domain 15) (Metalloproteinase-like, disintegrin-like, and cysteine-
DE rich protein 15) (MDC-15) (Metalloprotease RGD disintegrin protein)
DE (Metarigidin).
DE ADAM15 OR MDC15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Breast carcinoma;
RX MEDLINE=96214870; PubMed=8617717;
RA Knaetzschmar J., Lum L., Blobel C.P.;
RT "Metarigidin, a membrane-anchored metalloprotease-disintegrin protein
RT with an RGD integrin binding sequence.";
RL J. Biol. Chem. 271:4593-4596(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Umbilical vein;
RX MEDLINE=97192141; PubMed=9039960;
RA Herren B., Raines E.W., Ross R.;
RT "Expression of a disintegrin-like protein in cultured human vascular
RT cells and in vivo.";
RL PASRB J. 11:173-180(1997).
RN [3]
RP SEQUENCE FROM N.A.
RA Karkkainen I., Hovvila A.-P.J.;
RT "The characterization of human ADAM15 gene structure and promoter
RT region.";
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg H., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uesdin T.B., Toshynski S., Cantinot P., Prange C.J.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hilyk S.W.,
RA Villalón D.K., Muzey D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fabry J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Rodtgerfeld Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Schercher A., Schein J.E., Jones S.J.M., Marva M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RA human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP INTERACTION WITH INTEGRIN ALPHA-BETA3.
RX MEDLINE=98184837; PubMed=9516430;

RA Zhang X.P., Kamata T., Yokoyama K., Puzon-McLaughlin W., Takada Y.,
 RT "Specific interaction of the recombinant disintegrin-like domain of
 RT MDC-15 (metastatin, ADAM-15) with integrin alphavbeta3.";
 RL J. Biol. Chem. 273:7345-7350 (1998).
 RA [6]
 RP PHOSPHORYLATION OF TYR-715 AND TYR-735.
 RX MEDLINE=21826475; PubMed=11741929;
 RA Poghoyan Z., Robbins S.M., Houslay M.D., Webster A., Murphy G.,
 RA Edwards D.R.;
 RT "Phosphorylation-dependent interactions between ADAM15 cytoplasmic
 domain and Src family protein-tyrosine kinases.";
 RL J. Biol. Chem. 277:4999-5007 (2002).
 CC -1- FUNCTION: May be involved in cell-surface proteolysis, cell
 CC adhesion or intracellular protein maturation.
 CC -1- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
 CC -1- SUBUNIT: Interacts with ITGA9-ITGB3 (Vitellogenin receptor),
 CC PACSIN3 and SNX9. PACSIN3 and SNX9 preferentially bind the
 CC precursor but not the processed form of ADAM15, suggesting that
 CC the interaction occurs in a secretory pathway compartment prior to
 CC the medial Golgi (By similarity). Interacts specifically with Src
 CC family protein-tyrosine kinases (PTKs).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED. OVEREXPRESSED IN
 CC ARTERIOSCLECTOTIC LESIONS. CONSTITUTIVELY EXPRESSED IN CULTURED
 CC ENDOTHELIAL AND SMOOTH MUSCLE.
 CC -1- DOMAIN: THE CYTOPLASMIC DOMAIN INTERACTS WITH ENDOPHILIN I AND
 CC SORTING NEXIN 9 (By similarity).
 CC -1- DOMAIN: DESINTEGRIN DOMAIN BINDS TO INTEGRIN ALPHA9V-BETA3.
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- PTM: Phosphorylation increases association with PTKs.
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
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 CC -----
 DR EMBL: U46005; AACSI112.1; -;
 DR EMBL: U41767; AACSO404.1; -;
 DR EMBL: AF314227; AAM4189.1; -;
 DR EMBL: BC014566; AAM41566.1; -;
 DR HSSP: P18619; 1FVL.
 DR MEROPS: M12.215; -;
 DR GeneW: HGNC:193; ADAM15.
 DR MIM: 605548; -;
 DR GO: GO:0007160; P:cell-matrix adhesion; TAS.
 DR InterPro: IPR006586; ADM-Cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF-like.
 DR InterPro: IPR001818; Matrxin.
 DR InterPro: IPR002870; Pep_M12B_propep.
 DR InterPro: IPR001590; Repolysin.
 DR InterPro: IPR006025; Zn_Mtpeptidase.
 DR Pfam: PF00200; disintegrin; 1.
 DR Pfam: PF01562; Pep_M12B_propep; 1.
 DR Pfam: PF01421; Repolysin; 1.
 DR ProDom: PD000664; Disintegrin; 1.
 DR SMART: SM00608; ACR_1.
 DR SMART: SM00609; DISIN; 1.
 DR PROSITE: PS50215; ADM_MERO; 1.
 DR PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS00022; EGF_1; FALSE_NEG.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 DR Hydrolase; Metalloprotease; Zinc; signal; Glycoprotein; Zymogen;

KW Transmembrane; EGF-like domain; SH3-binding; Phosphorylation.
 FT SIGNAL 1 17
 FT PROPEP 18 206
 FT CHAIN 207 814
 FT DOMAIN 207 696
 FT TRANSMEM 697 717
 FT DOMAIN 718 814
 FT DOMAIN 207 414
 FT DOMAIN 421 508
 FT DOMAIN 509 656
 FT DOMAIN 657 685
 FT SITE 766 772
 FT SITE 801 807
 FT SITE 179 179
 FT SITE 484 486
 FT METAL 348 348
 FT ACT_SITE 349 349
 FT METAL 352 352
 FT METAL 358 358
 FT DISULFID 323 409
 FT DISULFID 480 493
 FT DISULFID 657 667
 FT DISULFID 661 673
 FT DISULFID 675 684
 FT MOD_RES 715 715
 FT MOD_RES 735 735
 FT CARBOHYD 389 389
 FT CARBOHYD 392 392
 FT CARBOHYD 606 606
 FT CARBOHYD 611 611
 FT CONFLICT 714 714
 FT CONFLICT 791 791
 SQ SEQUENCE 814 AA; 87716 MW; 683A8368AD30996B CRC64;
 Query Match 43.5%; Score 274; DB 1; Length 814;
 Best Local Similarity 48.5%; Pred. No. 4e-16;
 Matches 50; Conservative 11; Mismatches 32; Indels 10; Gaps 4;
 Oy 10 CGNGYVENGECDDGFGHVECYGLCCKK--GSLNSGANC-SNGPCNNNTSLCFORGVCYCR 66
 Db 424 CGNMFVEBEGQCDGFGFDDCDPCCDSLTCLRGAGACASGGPCCN--COLRPSGWQCR 481
 Oy 67 DAVNECDITTEYCTDSGGCCPNLHKDGYACNQNO----GRC 104
 Db 482 PTRGDCDLPFCFPPDSGCCPPDVSLGDEFPAGGAVCMGRG 524
 RESULT 10
 AD33_MOUSE STANDARD: PRT: 797 AA.
 AC Q923W9;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM_33 precursor (BC 3.4.24.-) (A disintegrin and
 DE metalloprotease domain 33).
 GN ADAM33.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC TISSUE=Brain;
 RX MEDLINE=21674006; PubMed=11814695;
 RA Yoshinaka T., Nishii K., Yamada K., Sawada H., Nishiwaki E., Smith K.,
 RA Yoshino K., Ishiguro H., Higashiyama S.;
 RT "Identification and characterization of novel mouse and human ADAM33s
 RT with potential metalloprotease activity.";
 RL Gene 282:227-236 (2002).
 RN (2)
 RP SEQUENCE OF 113-797 FROM N.A. (ISOFORM 1).

CC STRAIN=Swiss Webster / NIH;
 RA Smith K.M., Alfandari D., White J.M., Sutherland A.E., Desimone D.W.;
 RT "M-ADAM3 cloned from mouse embryo day 11 cDNA library."
 RL Submitted (MAY-2001) to the EMBL/Genbank/DBA databases.
 CC -1- COPROCTOR: BINDS ONE ZINC ION (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q923W9-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q923W9-2; Sequence=VSP_005496;
 CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FORIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 CC EMBL, AB059633; BAB84337.1; -;
 CC EMBL, AB059632; BAB84336.1; -;
 CC EMBL, AF366072; AAK67164.1; -;
 CC MGD, MG1:141813; Adam33.
 CC GO, GO:0016021; C:Integral to membrane; NAS.
 CC GO, GO:0004222; F:metalloendopeptidase activity; NAS.
 CC GO, GO:0008270; F:zinc ion binding activity; NAS.
 CC GO, GO:0006508; P:proteolysis and peptidolysis; NAS.
 CC GO, GO:004127; P:regulation of cell proliferation; NAS.
 CC GO, GO:0042035; P:regulation of cytokine biosynthesis; NAS.
 CC InterPro: IPR006586; ADAM_cysteine.
 CC InterPro: IPR001762; Disintegrin.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR001818; Matrxin.
 CC InterPro: IPR002870; Pep_M12B_propep.
 CC InterPro: IPR001580; Repolysin.
 CC InterPro: IPR006025; Zn_MTPeptidse.
 CC Pfam, PF00200; disintegrin; 1.
 CC Pfam, PF01562; Pep_M12B_propep; 1.
 CC Pfam, PF01421; Repolysin; 1.
 CC PRINTS: PR00289; DISINTEGRIN.
 CC ProDom, PD000664; Disintegrin; 1.
 CC SMART, SM00608; ACR; 1.
 CC SMART, SM00605; DISIN; 1.
 CC PROSITE, PS00215; ADAM_MPRO; 1.
 CC PROSITE, PS00546; CYSTEINE_SWITCH; FALSE_NEG.
 CC PROSITE, PS00427; DISINTEGRIN_1; FALSE_NEG.
 CC PROSITE, PS50214; DISINTEGRIN_2; 1.
 CC PROSITE, PS00022; EGF_1; FALSE_NEG.
 CC PROSITE, PS00186; EGF_2; 1.
 CC PROSITE, PS00142; ZINC_PROTEASE; 1.
 CC HydroLase: Metalloprotease; Zinc; Signal: Glycoprotein; Zymogen;
 KW Transmembrane; EGF-like domain; Alternative splicing.
 FT SIGNAL 1 29
 FT PROPEP 1 30
 FT CHAIN 205 797
 FT DOMAIN 30 702
 FT TRANSMEM 703 723
 FT DOMAIN 724 797
 FT DOMAIN 205 410
 FT DOMAIN 418 503
 FT DOMAIN 504 649
 FT DOMAIN 650 682
 FT DOMAIN 767 772
 FT SITE 134 134
 FT SITE 346 346
 FT METAL 347
 FT ACT_SITE 347

FT METAL 350 350 ZINC (CATALYTIC) (BY SIMILARITY).
 FT METAL 356 356 ZINC (CATALYTIC) (BY SIMILARITY).
 FT DISULFID 321 405 BY SIMILARITY.
 FT DISULFID 351 389 BY SIMILARITY.
 FT DISULFID 476 489 POTENTIAL.
 FT DISULFID 654 664 BY SIMILARITY.
 FT DISULFID 658 670 BY SIMILARITY.
 FT DISULFID 672 681 BY SIMILARITY.
 FT VARSPLIC 637 662 Missing (in isoform 2).
 FT FTId=VSP_005496
 FT CONFLICT 319 326 GICRAESS -> DMRGLSF (IN REF. 2).
 FT CONFLICT 725 725 MISSING (IN REF. 2).
 FT SEQUENCE 797 AA; 86954 MW; E405FC1B52C65FF CRC64;
 SQ
 Query Match 42.7%; Score 269; DB 1; Length 797;
 Best Local Similarity 45.3%; Pred. No. 1e-15; Indels 4; Gaps 2;
 Matches 48; Conservative 14; Mismatches 40;
 QY 1 PTKLPEPTCGNGVYAGREDCGFHVECYGLCC--KKCSLSNGAHCSGPPCCNNTSCLF 58
 DB 412 PGLVLPRCGNGFLEAGEBCDCGSGQKCPDPCFPHNCSLRAGNCAHGDCC--ARCLL 469
 QY 59 QPRGECRDVAVNCDITYCTGDSGQCPNHLKQDGYACNQNQRC 104
 DB 470 KSAQPCRPATDCLPBFCTGTSPYCPADVYLLDGSFCAGRGVC 515

Search completed: October 21, 2003, 10:06:24
 UoD time : 19.3145 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 21, 2003, 09:53:36 ; Search time 72.6038 Seconds
(without alignments)
369.643 Million calls updates/sec

Title: US-09-634-252a-4_COPY_496_599

Perfect score: 630
Sequence: 1 PRTLFEPTCEGNGVGEAGE.....CPNLHKQDGYANORQGRG 104

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	630	100.0	832	4	075077
2	611	97.0	690	11	08CC33
3	611	97.0	829	11	09RIV7
4	292	46.3	812	4	08N0W6
5	283	44.9	617	13	090499
6	276.5	43.9	587	5	08T319
7	276.5	43.9	959	5	09VPH0
8	275	43.7	451	13	09PT49
9	274	43.5	814	4	096C78
10	269	42.7	797	11	08R465
11	269	42.7	797	11	08R5G5
12	267.5	42.5	790	4	08T827
13	263	41.7	609	13	08UTN1
14	263	41.7	809	11	08CA82
15	263	41.7	864	11	08C720
16	259.5	41.2	1023	5	0967H9

17	259	41.1	914	13	012960	012960 xenopus lae
18	258	41.0	610	13	09Y120	09Y120 agkistrodon
19	258	41.0	836	6	019057	019057 pongo pygma
20	255	40.5	609	13	090282	090282 crocatus at
21	255	40.5	620	13	042138	042138 agkistrodon
22	254	40.3	212	13	090Y44	090Y44 agkistrodon
23	254	40.3	609	13	09W6M5	09W6M5 agkistrodon
24	254	40.3	610	13	093523	093523 bothrops ja
25	254	40.3	610	13	08QC88	08QC88 bothrops in
26	252.5	40.1	600	13	09PVK7	09PVK7 naja naja l
27	251	39.8	612	13	08UVG0	08UVG0 bothrops er
28	251	39.8	804	11	060410	060410 cavia porce
29	249	39.5	180	13	093518	093518 agkistrodon
30	249	39.5	899	13	08UVF1	08UVF1 coturnix co
31	247.5	39.3	655	4	08NFM6	08NFM6 homo sapien
32	247	39.2	761	11	08CDV3	08CDV3 mus musculu
33	246.5	39.1	845	11	061072	061072 mus musculu
34	246	39.0	614	13	08J1R1	08J1R1 trimeresuru
35	245.5	39.0	702	11	08BMR5	08BMR5 mus musculu
36	245.5	39.0	714	11	08K4K0	08K4K0 mus musculu
37	245.5	39.0	873	13	042595	042595 xenopus lae
38	245	38.9	604	13	09PT48	09PT48 atractaspis
39	244.5	38.8	610	13	08AW15	08AW15 agkistrodon
40	244.5	38.8	612	13	090213	090213 trimeresuru
41	244	38.7	606	13	098UFP9	098UFP9 bothrops ja
42	244	38.7	694	5	09GZ15	09GZ15 drosophila
43	244	38.7	791	11	060813	060813 mus musculu
44	244	38.7	1182	5	09VX11	09VX11 drosophila
45	243	38.6	216	13	09PSN7	09PSN7 crocatus ru

ALIGNMENTS

RESULT 1
ID 075077 PRELIMINARY; PRT; 832 AA.
AC 075077;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE MDC3 (ADAM22 protein).
GN ADAM22.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=98359734; PubMed=9693107;
RA Sagan K., Ohya Y., Hasegawa Y., Tanaka I.;
RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
RT and MDC3: novel human cellular disintegrins highly expressed in the
RT brain.";
RT Biochem. J. 334:93-98(1998).
RL [2]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC Cal S., Lopez-Otin C.;
RT "Identification and characterization of ADAM 22, a novel
RT metalloproteinase/disintegrin protein.";
RL Submitted (Apr-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB009672; BAA32351.1; -;
DR EMBL; AJ005580; CAC20565.1; -;
DR HSSP; P18619; 1FVL.
DR MEROPS; M12.979; -;
DR Genew; HGNC:202; ADAM23.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002870; Pep_M12B_propep.

```
DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Peg_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SO SEQUENCE 832 AA; 91925 MW; 7841A9670E1C24EF CRC64;

Query Match
Best Local Similarity 100.0%; Score 630; DB 4; Length 832;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 PTKLFEPTCEGNGYVAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFOP 60
DB 496 PTKLFEPTCEGNGYVAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFOP 555
61 RGYECRDVAVNECDITTEYCTGDSGQCPNHLKODGYACNONGRC 104
556 RGYECRDVAVNECDITTEYCTGDSGQCPNHLKODGYACNONGRC 599

RESULT 2
O8CC33 PRELIMINARY; PRT; 690 AA.
AC O8CC33.
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DE A disintegrin and metalloprotease domain 23.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Dienccephalon;
RX MEDLINE=22354683; PubMed=12466851;
RA The FANTOM Consortium,
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs."
RL Nature 420:563-573(2002).
DR EMBL; AK034022; BAC28550.1; -.
SO SEQUENCE 690 AA; 77228 MW; B61699141AECA6A6 CRC64;

Query Match
Best Local Similarity 97.0%; Score 611; DB 11; Length 690;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PTKLFEPTCEGNGYVAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFOP 60
DB 493 PTKLFEPTCEGNGYVAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFOS 552
61 RGYECRDVAVNECDITTEYCTGDSGQCPNHLKODGYACNONGRC 104
553 RGYECRDVAVNECDITTEYCTGDSGQCPNHLKODGYACNONGRC 596

RESULT 3
O9R1V7 PRELIMINARY; PRT; 829 AA.
AC O9R1V7.
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADAM23.
GN ADAM23.
OS Mus musculus (Mouse).
```

```
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=99365303; PubMed=10433968;
RA Sagane K., Yamazaki K., Mizui Y., Tanaka I.;
RT "Cloning and chromosomal mapping of mouse ADAM11, ADAM22 and ADAM23."
RL Gene 236:79-86(1999)
DR EMBL; AB009673; BAA83381.1; -.
DR HSSP; P18619; IFLV.
DR MEROPS; M12.979; -.
DR MGD; MGI:1345162; Adam23.
DR InterPro; IPR006586; ADAM_cysteine.
DR InterPro; IPR001762; Disintegrin.
DR InterPro; IPR006209; EGF-like.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002870; Peg_M12B_propep.
DR InterPro; IPR001590; Reprolysin.
DR Pfam; PF00200; disintegrin; 1.
DR Pfam; PF01562; Peg_M12B_propep; 1.
DR Pfam; PF01421; Reprolysin; 1.
DR ProDom; PD000664; Disintegrin; 1.
DR SMART; SM00608; ACR; 1.
DR SMART; SM00050; DISIN; 1.
DR SMART; SM00181; EGF; 1.
DR PROSITE; PS50215; ADAM_MERO; 1.
DR PROSITE; PS50214; DISINTEGRIN_2; 1.
DR PROSITE; PS00022; EGF_1; 1.
SO SEQUENCE 829 AA; 91547 MW; FE6BCD69DD50F53A CRC64;

Query Match
Best Local Similarity 96.2%; Score 611; DB 11; Length 829;
Matches 100; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 PTKLFEPTCEGNGYVAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFOP 60
DB 493 PTKLFEPTCEGNGYVAGEECDCGFHVCEYGLCKCKCSLSNGAHCSDPCCNNTSCLFOS 552
61 RGYECRDVAVNECDITTEYCTGDSGQCPNHLKODGYACNONGRC 104
553 RGYECRDVAVNECDITTEYCTGDSGQCPNHLKODGYACNONGRC 596

RESULT 4
O8N0W6 PRELIMINARY; PRT; 812 AA.
AC O8N0W6.
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE A disintegrin and metalloprotease domain 33.
GN ADAM33.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=uterus;
RX MEDLINE=22136089; PubMed=12110844;
RA Van Berdeghem P., Little R.D., Dupuis J., Del Mastro R.G., Falls K.,
RA Simon J., Torrey D., Pandit S., McKenny J., Braunschweiger K.,
RA Walsh A., Liu Z., Hayward B., Folz C., Manning S.P., Bawa A.,
RA Sarachin L., Thackston M., Benchekroun Y., Capparelli N., Wang M.,
RA Adair R., Feng Y., Dubois J., Fitzgerald M.G., Huang H., Gibson R.,
RA Allen K.M., Pedan A., Danzig M.R., Umland S.P., Egan R.W., Cuss F.M.,
RA Roke S., Clough J.B., Holloway J.W., Holgate S.T., Keith T.P.;
RT "Association of the ADAM33 gene with asthma and bronchial
RT hypersponsiveness."
RL Nature 418:426-430(2002).
DR EMBL; AF466287; AAM80482.1; -.
```


DR EMBL, AF466288; AAM80483.1; -
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR002870; Pep_M12B_propep.
 DR InterPro: IPR001590; Reptolysin.
 DR InterPro: IPR006025; Zn_MTPetase.
 DR Pfam: PF00200; disintegrin_1.
 DR Pfam: PF01562; Pep_M12B_propep_1.
 DR Pfam: PF01421; Reptolysin_1.
 DR PRINTS: PR00289; DISINTEGRIN.
 DR ProDom: PD000664; disintegrin_1.
 DR SMART: SM00608; ACR_1.
 DR SMART: SM00050; DISIN_1.
 DR PROSITE: PS50215; ADAM_MERO_1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR InterPro: Metalloprotease; Protease.
 KW SEQUENCE 812 AA; 87667 MW; EBA817363E2489EC CRC64;

Query Match 46.3%; Score 292; DB 4; Length 612;
 Best Local Similarity 51.0%; Pred. No. 1.1e-26;
 Matches 51; Conservative 11; Mismatches 34; Indels 4; Gaps 2;

QY 7 PTECGNGVGEAGEECDCGFHVECYGLCC--KKCSLSNGAHCSGDPCCNNTSCLFQPRGYE 64
 DB 417 PALCGNGFVEAGEECDCGPGEGCDLCCFANHCSLRFAGCAQAHDC--VRCCLKPAGAL 474
 QY 65 CRDAVNECDITVEYTGSGGCGPPNHLKODGYACNONGRC 104
 DB 475 CROMAGDCDLPEFCTGSHCPDVPVYLDGSPCARSGGYC 514

RESULT 5

ID Q90499 PRELIMINARY; PRT; 617 AA.
 AC Q90499;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Metalloprotease.
 GN ECHI.
 OS Echis pyramidum (carpet viper).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubridae;
 OC Viperidae; Viperinae; Echis.
 NC NCB1_TaxID=8700;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Venom gland;
 RX MEDLINE=95010025; PubMed=7925363;
 RA Payne M.J.I., Moura Da-Silva A.M., Theakston R.D.G., Creighton J.M.;
 RT "Cloning of metalloprotease genes in the carpet viper (Echis pyramidum
 RT laevis). Further members of the metalloprotease/disintegrin gene
 RT family";
 RL Eur. J. Biochem. 224:483-488(1994).
 DR EMBL: X78970; CA55565.1; -
 DR HSSP: P18619; 1FVL.
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR002870; Pep_M12B_propep.
 DR InterPro: IPR001590; Reptolysin.
 DR InterPro: IPR006025; Zn_MTPetase.
 DR Pfam: PF00200; disintegrin_1.
 DR Pfam: PF01562; Pep_M12B_propep_1.
 DR Pfam: PF01421; Reptolysin_1.
 DR PRINTS: PR00289; DISINTEGRIN.
 DR ProDom: PD000664; disintegrin_1.
 DR SMART: SM00608; ACR_1.
 DR SMART: SM00050; DISIN_1.
 DR PROSITE: PS50215; ADAM_MERO_1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00427; DISINTEGRIN_1; 1.

DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 KW Protease.
 FT CHAIN 193 617 METALLOPROTEASE.
 SQ SEQUENCE 617 AA; 69310 MW; 83DCDAS4F43AFBA CRC64;

Query Match 44.9%; Score 283; DB 13; Length 617;
 Best Local Similarity 44.8%; Pred. No. 9.8e-26;
 Matches 47; Conservative 17; Mismatches 37; Indels 4; Gaps 2;

QY 2 TKLFPEPCGNGVGEAGEECDCGFHVECYGLCC--KCSLSNGAHCSGDPCCNNTSCLFQ 59
 DB 399 TDIVSPGCGNYFVEAGEECDCGRTYCRNPCCNATTKLTPGSCADGECCN--QCRFR 456
 QY 60 PRGYECRDANVEDITVEYTGSGGCGPPNHLKODGYACNONGRC 104
 DB 457 PARTCCRKIDCDVPEYCTGSGCEPLDVFRNGPYQSNNGYC 501

RESULT 6

ID Q87319 PRELIMINARY; PRT; 587 AA.
 AC Q87319;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE S003917D.
 GN CG31314 OR CG7649.
 OS Drosophila melanogaster (fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY05096; AAM11424.1; -
 DR FLYBase: FBgn0051314; CG31314.
 DR InterPro: IPR006586; ADAM_cysteine.
 DR InterPro: IPR001762; Disintegrin.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001590; Reptolysin.
 DR InterPro: IPR006025; Zn_MTPetase.
 DR Pfam: PF00200; disintegrin_1.
 DR Pfam: PF01421; Reptolysin_1.
 DR ProDom: PD000664; disintegrin_1.
 DR SMART: SM00608; ACR_1.
 DR SMART: SM00050; DISIN_1.
 DR PROSITE: PS50215; ADAM_MERO_1.
 DR PROSITE: PS50214; DISINTEGRIN_2; 1.
 DR PROSITE: PS00022; EGF_1; 1.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 DR PROSITE: PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 587 AA; 63507 MW; 3D910ADF283365DB CRC64;

Query Match 43.9%; Score 276.5; DB 5; Length 587;
 Best Local Similarity 45.8%; Pred. No. 5.7e-25;
 Matches 49; Conservative 16; Mismatches 39; Indels 3; Gaps 2;

QY 1 PTKLFPEPCGNGVGEAGEECDCGFHVECYGLCC--KKCSLSNGAHCSGDPCCNNTSCLFQ 57
 DB 76 PERLFSPGCGNGVGEAGEECDCGLRPHNCNACNQTCLHNSKATCATGECDDLTTCR 135
 QY 58 FQPRGYECRDANVEDITVEYTGSGGCGPPNHLKODGYACNONGRC 104
 DB 136 PKLAGSACREANECDLPEYCTGSEYCPADVFRFRDTEPCDGGQAYC 182

RESULT 7
 Q9VFH0 PRELIMINARY: PRT: 959 AA.
 ID Q9VFH0
 AC Q9VFH0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-OCT-2000 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE CG31314 protein.
 GN CG31314 OR CG7649.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 [1]
 RN SEQUENCE FROM N.A.
 RP STRAIN=Berkely;
 RC MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scher S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champagne M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abill J.F., Agbayani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Ballew R.M., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brockstein P., Brottier P.,
 RA Butris K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doug L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glaser K.,
 RA Glodek A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laaso P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Modyaty C., Morris J., Moshireli A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Relbert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strongs R., Sun E.,
 RA Svrtskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Weissman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 "The genome sequence of Drosophila melanogaster";
 Science 287:2185-2195 (2000).
 [2]
 RN SEQUENCE FROM N.A.
 RP Celinker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Barton J., An H., Baldwin D., Banzon J., Beeson K.Y., Busan D.A.,
 RA Carlson J.W., Center A., Champagne M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doug L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Fries E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshireli A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
 RA Pacieb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouanavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svrtskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 "Sequencing of Drosophila melanogaster genome";

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celinker S.E.,
 RA Krommiller B., Marschall B., Milburn G., Richter J., Russo S.,
 RA Seale S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RT "Annotation of Drosophila melanogaster genome";
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Celinker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RN Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Flybase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AE003705; AAF55088.2; -
 DR HSSP; P18619; 1FVL.
 DR Flybase; FBgn0051314; CG31314.
 DR InterPro; IPR001762; Disintegrin.
 DR InterPro; IPR006209; EGF-like.
 DR InterPro; IPR002870; PEP_M12B.
 DR InterPro; IPR001590; Reprolysin.
 DR InterPro; IPR006025; Zn_MTPepidase.
 DR Pfam; PF00200; disintegrin_1.
 DR Pfam; PF01562; PEP_M12B_propep_1.
 DR Pfam; PF01421; Reprolysin_1.
 DR ProDom; PD000664; Disintegrin_1.
 DR SMART; SM00050; DISIN; 1.
 DR PROSITE; PS50215; ADAM_MEPPO; 1.
 DR PROSITE; PS50214; DISINTEGRIN_2; 1.
 DR PROSITE; PS00022; EGF_1; 1.
 DR PROSITE; PS01186; EGF_2; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 DR PROSITE; PS00142; ZINC_PROTEASE; 1.
 SQ SEQUENCE 959 AA; 105329 MW; E60F9309F4ACE3C6 CRC64;
 Query Match 43.9%; Score 276.5; DB 5; Length 959;
 Best Local Similarity 45.8%; Pred. No. 9.3e-25;
 Matches 49; Conservative 16; Mismatches 39; Indels 3; Gaps 2;
 QY 1 PTKLPEPFCNGYVEAGECDGCFHVECYGLCC--KKCSF-SNGAHGSDGPCNNNTSCL 57
 DB 448 PERLPFESTCGNGFVPEPEQDCDGLPEHCENACCAQTCMLHSHKATCATGECDDTTTCR 507
 QY 58 FQPRGCEGRDAVNECDITEYCTGDSGQCPNVLHKQDGYACNQNQGRG 104
 DB 508 PKLAGSACREABNECDLPEYCTGSESEYCPADVFRDTEPCDGGQAYC 554
 RESULT 8
 Q9PT49 PRELIMINARY: PRT: 451 AA.
 ID Q9PT49
 AC Q9PT49
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Metalloproteinase precursor (Fragment).
 OS Atractaspis engaddensis (Israeli burrowing asp).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidodonta; Squamata; Scieroglossa; Serpentes; Colubroidae;
 OC Atractaspididae; Atractaspis.
 NCBI_TaxID=8600;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=venom gland;
 RA Duencel F.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF186368; AAF01040.1; -
 DR HSSP; P18619; 1FVL.

DR InterPro: IPR006586; ADAM_cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR001590; Reptolysin.
DR InterPro: IPR006025; Zn_MTPepdse.
DR Pfam: PF00200; disintegrin_1.
DR Pfam: PF01421; Reptolysin_1.
DR ProDom: PD000664; Disintegrin_1.
DR SMART: SM00608; ACR_1.
DR SMART: SM00505; DISIN_1.
DR PROSITE: PS50215; ADAM_MERPRO_1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
DR Signal.
KW NON_TER 1 1 POTENTIAL.
FT SIGNAL <1 2 METALLOPROTEINASE.
FT CHAIN 31 235 DISINTEGRIN.
FT CHAIN 236 328
SQ SEQUENCE 451 AA; 50286 MW; 8C1395BF9B9D3EF8 CRC64;
Query Match 43.7%; Score 275; DB 13; Length 451;
Best Local Similarity 48.0%; Pred. No. 6.6e-25;
Matches 48; Conservative 11; Mismatches 37; Indels 4; Gaps 2;
QY 7 PTEGNGVYVGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLFOPRGVE 64
DB 243 PAVGNGVYVGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLFOPRGVE 64
QY 65 CRDAVNECDITETCTGDSGCGCPNHLKODGYACNONGRC 104
DB 301 CRAMDECDPELCTGDSGCGCPNHLKODGYACNONGRC 340
RESULT 9
Q96C78 PRELIMINARY; PRT; 814 AA.
AC Q96C78
DT 01-DEC-2001 (TRENBLrel. 19, Created)
DT 01-DEC-2001 (TRENBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE A disintegrin and metalloproteinase domain 15 (metargidin)
DE (Metalloprotease disintegrin).
GN ADAM15.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strauberg R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Karkkainen I., Huovila A.-P.J.;
RT "The characterization of human ADAM15 gene structure and promoter
region."
RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
DB EMBL: BC014566; AAM44566.1; -
DB EMBL: AF314227; AAM44189.1; -
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006029; EGF_like.
DR InterPro: IPR002870; Pep_M12B_propep.
DR InterPro: IPR001590; Reptolysin.
DR InterPro: IPR006025; Zn_MTPepdse.
DR Pfam: PF00200; disintegrin_1.
DR Pfam: PF01562; Pep_M12B_propep; 1.
DR Pfam: PF01421; Reptolysin_1.
DR ProDom: PD000664; Disintegrin_1.
DR PROSITE: PS50215; ADAM_MERPRO_1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Integrin; Protease.

SQ SEQUENCE 814 AA; 87717 MW; 683AB368AD30996B CRC64;
Query Match 43.5%; Score 274; DB 4; Length 814;
Best Local Similarity 48.5%; Pred. No. 1.6e-24;
Matches 50; Conservative 11; Mismatches 32; Indels 10; Gaps 4;
QY 10 CGNGVYVGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLFOPRGVECR 66
DB 424 CGNMFVYVGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLFOPRGVECR 66
QY 67 DAVNECDITETCTGDSGCGCPNHLKODGYACNONGRC 104
DB 482 PTRGDCDLPEFCPPDSSGCGCPNHLKODGYACNONGRC 524
RESULT 10
Q96C78 PRELIMINARY; PRT; 797 AA.
AC Q96C78
DT 01-JUN-2002 (TRENBLrel. 21, Created)
DT 01-JUN-2002 (TRENBLrel. 21, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE ADAM33.
GN ADAM33.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H/HeJ;
RA Gunn T.M., Azarani A., Kim P., Hyman R.W., Davis R.W., Barsh G.S.;
RT "Identification and preliminary characterization of mouse Adam33."
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
DB EMBL: AY054984; AAL14350.1; -
DR MGD: MGI:1341813; Adam33.
DR InterPro: IPR006586; ADAM_cysteine.
DR InterPro: IPR001762; Disintegrin.
DR InterPro: IPR006029; EGF_like.
DR InterPro: IPR002870; Pep_M12B_propep.
DR InterPro: IPR001590; Reptolysin.
DR InterPro: IPR006025; Zn_MTPepdse.
DR Pfam: PF01562; Pep_M12B_propep; 1.
DR Pfam: PF01421; Reptolysin_1.
DR ProDom: PD000664; Disintegrin_1.
DR SMART: SM00608; ACR_1.
DR SMART: SM00505; DISIN_1.
DR PROSITE: PS50215; ADAM_MERPRO_1.
DR PROSITE: PS50214; DISINTEGRIN_2; 1.
DR PROSITE: PS01186; EGF_2; 1.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
SQ SEQUENCE 797 AA; 87009 MW; C805B5FFD87E3E CRC64;
Query Match 42.7%; Score 269; DB 11; Length 797;
Best Local Similarity 45.3%; Pred. No. 6.2e-24;
Matches 48; Conservative 14; Mismatches 40; Indels 4; Gaps 2;
QY 1 PTKLPEPTGNGVYVGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLF 58
DB 412 PGLVLPLPRGNGVYVGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLF 58
QY 59 QPRVYVGEBCDGFHVECYGLCK--KCSLSNGAHSGDGPCCNNTSCLF 104
DB 470 KSAQTPCRPAATDCDLPEFCPPDSSGCGCPNHLKODGYACNONGRC 515

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